

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 15, 2004, 12:20:54 ; Search time 2978.97 Seconds
(without alignments)
11596.087 Million cell updates/sec

Title: US-09-931-704-1
Perfect score: 797
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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- 41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

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and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	797	100.0	797	6	AR002595	AR002595 Sequence
2	797	100.0	797	6	AX392086	AX392086 Sequence
3	797	100.0	797	6	BD195447	BD195447 The neuro
4	797	100.0	797	9	AF176911	AF176911 Homo sapi
5	793.4	99.5	881	6	AX205024	AX205024 Sequence
6	793.4	99.5	881	6	AX205042	AX205042 Sequence
7	776.4	97.4	1736	9	BC012939	BC012939 Homo sapi
8	749.4	94.0	1689	9	AF172854	AF172854 Homo sapi
9	749.4	94.0	1710	6	BD132824	BD132824 Cardiotro
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14	669.4	84.0	819	10	AF176913	AF176913 Mus muscu
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ALIGNMENTS

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DEFINITION	AR002595	Sequence 1 from patent US 5741772.	797 bp	DNA	linear	PAT 04-DEC-1998
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VERSION	AR002595.1	GI:3964149	797 bp	DNA	linear	PAT 04-DEC-1998
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 797)					
AUTHORS	Chang, M.-s.					
TITLE	Neurotrophic factor NNT-1					
JOURNAL	Patent: US 5741772-A 1 21-APR-1998;					
FEATURES	Location/Qualifiers					

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DEFINITION Sequence 1 from Patent WO0215977.
ACCESSION AX392086
VERSION AX392086.1 GI:19700574
KEYWORDS
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 Senaldi, G.
AUTHORS Methods and compositions for treating ige-related disease using nn
TITLE t-1 inhibitors
JOURNAL Patent: WO 0215977-A 1 28-FEB-2002;
Angen Inc. (US)
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ACCESSION BD195447
VERSION BD195447.1 GI:33005217
KEYWORDS JP 2002514067-A/1.
SOURCE unidentified
ORGANISM unidentified
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REFERENCE 1 (bases 1 to 797)
AUTHORS Chang,M.S., Elliott,G.S., Senaldi,G. and Sarmiento,U.
TITLE The neurotrophic factor NNT-1
JOURNAL Patent: JP 2002514067-A 1 14-MAY-2002;
AMGEN INC
COMMENT OS Unidentified
PN JP 2002514067-A/1
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PF 02-FEB-1998 JP 1998533258
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RESULT 4
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DEFINITION complete cds.
ACCESSION AF176911
VERSION AF176911.1 GI:6007640
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 797)
AUTHORS Senaldi,G., Varnum,B.C., Sarmiento,U., Starnes,C., Lile,J.,
Scully,S., Guo,J., Elliott,G., McNinch,J., Shaker,C.L.,
Freeman,D., Manu,F., Simonet,W.S., Boone,T. and Chang,M.S.
TITLE Novel neurotrophin-1/B cell-stimulating factor-3: a cytokine of the
IL-6 family
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (20), 11458-11463 (1999)
MEDLINE 99432254
PUBMED 10500198
REFERENCE 2 (bases 1 to 797)
AUTHORS Senaldi,G., Varnum,B., Sarmiento,U., Lile,J., Starnes,C.,
Scully,S., Guo,J., Elliott,G., McNinch,J., Freeman,D., Shaker,C.,
Manu,F., Simonet,W.S., Boone,T. and Chang,M.S.
TITLE Direct Submission
JOURNAL Submitted (11-AUG-1999) Amgen, Inc., One Amgen Center Drive,
Thousand Oaks, CA 91320, USA
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VERSION AX205024.1 GI:15394259
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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ORIGIN

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REFERENCE
AUTHORS Elson,G., Gauchat,J.F., Plun-Favreau,H., Chevalier,S. and Gascan,H.
TITLE Isolated complex comprising a nnt-1 protein and in addition at
JOURNAL least a clf-1 protein and/or a scntfr_g(a) protein
PIERRE: WO 0155172-A 1 02-AUG-2001.
PIERRE: FARE MEDICAMENT (FR); INSTITUT NATIONAL DE LA SANTE ET DE
LA RECHERCHE MEDICALE (INSERM) (FR)
FEATURES
source Location/Qualifiers
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Query Match 100.0%; Score 797; DB 9; Length 797;
Best Local Similarity 100.0%; Pred. No. 1.2e-152;
Matches 797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATTAAGCTTCGCGAGCGGGCTCGCCCTCCCACTCCGACAGGGGACTCGTGGGGA 60
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QY 241 AGCACAACTCCGACGTTGGTGGGACTATCTGAACCTACCTGGGCCCTTTCAACG 300
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QY 301 AGCCAGCTTCAACCTCCCGCTGGGGGAGAGACTCTGGGAGTCCGAGTGGGGA 360
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QY 421 GCACCTTCTGTGTTACTTGGTGGGCTCAACCGTTCAGGCTGCGACTGCTGAGTGG 480
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QY 721 CTCAGACCTGTGGGCTGCGGCTCGGCAAGGACTTCAACCGGCTCAAGAAAGATGACG 780
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Query Match 99.5%; Score 793.4; DB 6; Length 881;
Best Local Similarity 99.9%; Pred. No. 6.3e-152;
Matches 794; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db |||||

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Pahey, J., Helton, E., Kettelman, M., Madan, A., Young, A.C., Shevchenko, Y., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Dufford, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krywinski, M.I., Skalska, U., Smalhus, D.E., Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

22388257

12477932

2 (bases 1 to 1736)

Strausberg, R.

Direct Submission

Submitted (20-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgabs@mail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.

DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

Sequencing by: Baylor College of Medicine Human Genome Sequencing Center

Center code: BCM-HGSC

Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>

Contact: ang@bcm.tmc.edu

Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Ioulseseg, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAK Plate: 28 Row: b Column: 23

This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 7019350.

Location/Qualifiers

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Query Match 97.4%; Score 776.4; DB 9; Length 1736;

Best Local Similarity 99.9%; Pred. No. 1.7e-148;

Matches 777; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 78 AGCCCCAGCCCCATGGACCTCCGAGAGAGGAGACTCGTGGGGGATGTTAGCGTCCCTGTGC 137

DB 61 GGGCCAGCCCCATGGACCTCCGAGAGAGGAGACTCGTGGGGGATGTTAGCGTCCCTGTGC 120

QY 138 ACGGTGCTTGGCACTTCCCTGAGTGCAGCTCTCAATGCGACAGGGAGCCAGGGCCCT 197

DB 121 ACGGTGCTTGGCACTTCCCTGAGTGCAGCTCTCAATGCGACAGGGAGCCAGGGCCCT 180

QY 198 GGGCCCTCCATCCAGAAACCTATGACCTCACCCGCTACCTGGAGCAGCAACTCCGCGC 257

DB 181 GGGCCCTCCATCCAGAAACCTATGACCTCACCCGCTACCTGGAGCAGCAACTCCGCGC 240

QY 258 TTGGCTGGGACCTATCTGAATACCTTGGGCCCCCTTTCAAGAGCAGCACTTCAACCCCT 317

DB 241 TTGGCTGGGACCTATCTGAATACCTTGGGCCCCCTTTCAAGAGCAGCACTTCAACCCCT 300

QY 318 CCGCGCTGGGCGAGAGACTCTGCCAGGGCCACTGTTGACTTGGAGTGTGGCGAAGC 377

DB 301 CCGCGCTGGGCGAGAGACTCTGCCAGGGCCACTGTTGACTTGGAGTGTGGCGAAGC 360

QY 378 CTCAATGACAACTGGGGCTGACCCAGAACTACAGGGCCCTACAGCCACCTTCTGTGTAC 437

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QY 438 TTGGTGGCTTCAACCGTCAAGGCTGCAGCTGTGAGCTGGCGCGAGCCCTGGCCCACTTC 497

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RESULT 8

AF172854

LOCUS

DEFINITION

AF172854

ACCESSION

VERSION

AF172854.1

GI:5852980

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1689)

Shi, Y., Wang, W., Yourey, P.A., Gohari, S., Zukauskas, D., Zhang, J., Ruben, S., and Alderson, R.F.

Computational EST database analysis identifies a novel member of the neurotrophic cytokine family

Biochem. Biophys. Res. Commun. 262 (1), 132-138 (1999)

99382254

MEDLINE

10448081

FUNDED

REFERENCE

2 (bases 1 to 1689)

AUTHORS	Shi, Y.
TITLE	Direct Submission
JOURNAL	Submitted (28-JUL-1999) Molecular Biology, Human Genome Science, Inc., 9410 Key West Avenue, Rockville, MD 20850, USA
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Best Local Similarity	99.9%; Pred. No. 5.5e-143;
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Qy	105 GGGGACTCGTGGGGGATGTTAGCGTGCGTTGTGCAACGGTGCTCTGGCACCTCCCTCGAGTG 164
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Db	
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 DEFINITION Homo sapiens cardiotrophin-like cytokine (CLC) mRNA, complete cds.
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 VERSION AY049779.1 GI:16356642
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 680)
 AUTHORS Hu, X., Xu, Y., Zhang, B., Peng, X., Yuan, J. and Qiang, B.
 TITLE Direct Submission
 JOURNAL Submitted (30-JUL-2001) Department of Biochemistry, Institute of
 Basic Medical Science, Chinese Academy of Medical Sciences, 5 Dong
 Dan San Tiao, Beijing 100005, P.R. China

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ORIGIN

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 QY 148 GGCACCTCCCTGAGTGCAGCTCTCAATGCGACAGGGAGCCAGGGCTGCGCCCTCCA 207
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 QY 208 TCAGAAAACTATGACCTCACCCTGCTACCTGAGGACCAACTCCGACGCTTGGCTGGGA 267
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 ACCESSION AR002597
 VERSION AR002597.1 GI:3964151
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 819)
 AUTHORS Chang, M.-s.
 TITLE Neurotrophic factor NNT-1
 JOURNAL Patent: US 5741772-A 4 21-APR-1998;
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ORIGIN

Query Match 84.0%; Score 669.4; DB 6; Length 819;
 Best Local Similarity 92.0%; Pred. No. 1.3e-126;
 Matches 717; Conservative 0; Mismatches 61; Indels 1; Gaps 1;
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ACCESSION   BD195449
VERSION     BD195449.1
KEYWORDS    GI:33005219
SOURCE      JP 2002514067-A/3.
ORGANISM    unidentified
            unclassified.
REFERENCE   1 (bases 1 to 819)
AUTHORS    Chang, M.S., Elliott, G.S., Senaldi, G. and Sarmiento, U.
TITLE      The neurotrophin factor NNT-1
JOURNAL    Patent: JP 2002514067-A 3 14-MAY-2002;
            AMGEN INC
COMMENT     OS Unidentified
            PN JP 2002514067-A/3
            PD 14-MAY-2002
            PF 02-FEB-1998 JP 1998533258
            PR 03-FEB-1997 US 08/792019, 30-JAN-1998 US 09/016534 P1
            MING SHI CHANG, GARY S ELLIOTT, GIORGI SENALDI, ULJA SARMIENTO PC
            C12N15/18, C07K14/475, C07K16/22, C12N1/21, A61K38/18, A01K67/027 CC
            Strandedness: Single;
            CC Topology: Linear;
            CC The neurotrophic factor NNT-1
            FH Key Location/Qualifiers
            FT CDS 95..769
            FT mat peptide 176..1769
            FT sig peptide 95..175.
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FEATURES
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        1..819
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        Query Match 84.0%; Score 669.4; DB 6; Length 819;
        Best Local Similarity 92.0%; Pred. No. 1.3e-126;
        Matches 717; Conservative 0; Mismatches 61; Indels 1; Gaps 1;

QY 1 ATTAAGCTTCGCGAGCGGGCTCGCGCTCCCACTCCGACGCTCCGGAGGAGGAG 60
DB 1 ATTAAGCTTCGCGAGCGGGCTCGCGCTCCCACTCCGACGCTCCGGAGGAGGAG 64
QY 61 CGCACCCCGCGCGCCAG-CGCCAGCCATGAGACTCCGAGCGGGACTCGTGGGGG 119
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DB 125 ATGTTAGCTTGCTATGCAGCGTGTGTGGCACTCCCTCGAGTGCAGCTCTTAATGC 184
QY 180 ACAGGGGACCCAGGGCGCTGGCGCTCCATCCAGAAAACCTATGACTCACCGCTACCTG 239
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RESULT 14
LOCUS      AF176913
DEFINITION Mus musculus neurotrophin-1/B-cell stimulating factor-3 mRNA,
            complete cds.
ACCESSION  AF176913
VERSION    AF176913.1
KEYWORDS   GI:6007644
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
            1 (bases 1 to 819)
AUTHORS    Senaldi, G., Varnum, B.C., Sarmiento, U., Starnes, C., Lile, J.,
            Scully, S., Guo, J., Elliott, G., McNinch, J., Shaklee, C.L.,
            Freeman, D., Manu, F., Simonet, W.S., Boone, T. and Chang, M.S.
            Novel neurotrophin-1/B cell-stimulating factor-3: a cytokine of the
            IL-6 family
            Proc. Natl. Acad. Sci. U.S.A. 96 (20), 11458-11463 (1999)
JOURNAL    99432254
MEDLINE    10500198
REFERENCE   2 (bases 1 to 819)
AUTHORS    Senaldi, G., Varnum, B., Sarmiento, U., Lile, J., Starnes, C.,
            Scully, S., Guo, J., Elliott, G., McNinch, J., Freeman, D., Shaklee, C.,
            Manu, F., Simonet, W.S., Boone, T. and Chang, M.S.
            Direct Submission
            Submitted (11-AUG-1999) Amgen, Inc., One Amgen Center Drive,
            Thousand Oaks, CA 91320, USA
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        Matches 717; Conservative 0; Mismatches 61; Indels 1; Gaps 1;

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QY 720 CTTCCAGAGTGTGAGTCAACCTGACCTGGGGCTCATGGCTTCTGACTTCTGACCTT 778
Db 725 CTTCCAGAGTGTGAGTCAACCTGACCTGGGGCTCATGGCTTCTGACTTCTGACCTT 783

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RESULT 15
AX205060
LOCUS AX205060 1692 bp DNA linear PAT 30-AUG-2001
DEFINITION Sequence 19 from Patent WO0155219.
ACCESSION AX205060
VERSION AX205060.1 GI:15394299
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Elson, G. and Gauchat, J. F.
TITLE Scsntfr/mnt-1 fusion protein
JOURNAL Patent: WO 0155219-A 19 02-AUG-2001;
PIERRE FABRE MEDICAMENT (FR)
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ORIGIN

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Query Match 74.6%; Score 594.4; DB 6; Length 1692;
Best Local Similarity 98.2%; Pred. No. 2.5e-111;
Matches 601; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY 171 CTCATAGTCAGACGAGGACCCAGGCGCTGGCCCTCCATCCAGAAAACCTATGACCTCAC 230
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QY 231 CGCTACTCGAGACCAACTCCGACGCTTGGCTGGGACCTATCTGAACCTACCTGGGCCCC 290
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QY 411 GAGGCTCAGACCACTTCTGTGTTACTTGGCTGGGCTCAACCGTCAGGCTGCGCACTGCT 470
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Job time : 2983.97 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 15, 2004, 15:26:00 ; Search time 1814.21 Seconds
(without alignments)
13118.770 Million cell updates/sec

Title: US-09-931-704-1

Perfect score: 797

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Scoring table: IDENTITY_NUC

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Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

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28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	740.4	92.9	887	13	BQ948158
2	711.6	89.3	788	14	CF271927
3	706.8	88.7	787	14	CK130210
4	700	87.8	806	14	CK130211

5	698.6	87.7	804	14	CF271929
6	694.8	87.2	752	14	CF271925
7	684	85.8	810	14	CK130212
8	662	83.1	662	29	AY409170
9	656.4	82.4	1157	13	BQ940483
10	654	82.1	662	29	AY409171
11	647.2	81.2	800	14	CF271926
12	644.6	80.5	853	12	BG437538
13	621	77.9	1053	12	BG164929
14	604.8	75.9	801	14	CF271930
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16	590.8	74.1	594	12	BM763333
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18	576.4	72.3	678	13	BY735168
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22	549.8	69.0	634	13	EX497225
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34	379.8	47.7	448	13	BY531444
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ALIGNMENTS

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DEFINITION AGENCOURT_8813192 NIH_MGC_101 Homo sapiens cdna clone IMAGE:6428214
5', mRNA sequence.
ACCESSION BQ948158
VERSION BQ948158.1 GI:22363636
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 887)
AUTHORS NIH-MGC <http://mgc.ncl.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cdna Library Preparation: Rubin Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Cloned by: Agencourt Bioscience Corporation
Cloned through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LCM2614 row: h column: 07
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Qy	181	CAGGGAGCCAGCGGCTGCGCCCTCCATCCAGAAACCTATGACCTCACCGCTACCTGG	240
Db	188	CAGGGAGCCAGCGGCTGCGCCCTCCATCCAGAAACCTATGACCTCACCGCTACCTGG	247
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Qy	660	CTGACAGCTGGCTGGGCTCTGGCCAAAGGACTTCAACCGCTCAAGAAAGATGAG	719
Db	668	CTGACAGCTGGCTGGGCTCTGGCCAAAGGACTTCAACCGCTCAAGAAAGATGAG	727
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DEFINITION		AGENCOURT_15196974 NIH_MGC_195 Homo sapiens cDNA clone	
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ACCESSION		CF271927	
VERSION		2	
KEYWORDS		EST	
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ORGANISM		Homo sapiens	
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		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE		1 (bases 1 to 788)	
AUTHORS		NIH-MGC http://imgc.nci.nih.gov/	
TITLE		National Institutes of Health, Mammalian Gene Collection (MGC)	
JOURNAL		Unpublished (1999)	
COMMENT		On Aug 12, 2003 this sequence version replaced gi:33627839.	
		Contact: Daniela S. Gerhard, Ph.D.	
		Office of Cancer Genomics	
		National Cancer Institute / NIH	
		Bldg. 31 Rm10A07 Bethesda, MD 20892	
		Email: gcapbs@mail.nih.gov	
		Tissue Procurement: Narayan Bhat	
		cDNA Library Preparation: Bhat Laboratory	
		DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)	
		Clone distribution: MGC clone distribution information can be	
		found through the I.M.A.G.E. Consortium/LLNL at:	
		http://imgc.llnl.gov	
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		/note="Vector: pDNR-Dual; Site 1: loxp-Sall; Site 2: loxp-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxp sites of the pDNR-dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat a Note: this is a NIH_MGC Library."	
ORIGIN		89.3%; Score 711.6; DB 14; Length 788;	
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Matches 714; Conservative 0; Mismatches 4; Indels 0; Gaps 0;			
Qy	77	CAGCCCCAGCCCATGACCTCCGAGCAGGGGACTCGTGGGAGATGTTAGCGTGGCTGTG	136
Db	24	CAGTCCAGCGCCCCCATGACCTCCGAGCAGGGGACTCGTGGGAGATGTTAGCGTGGCTGTG	83
Qy	137	CACGGTGTCTGGCAGCTCCCTGTCAGTGGCAGCTCTCAATCCGACAGGGGACCCAGGGCC	196

Db	84	CACGGTGTCTGGCACCTCCCTGCAGTCCAGTCTCAATCGCACAGGGACCCAGGGCC	143
QY	197	TGGCCCTCCATCCAGAAACCTATGACCTACCCGCTACTCTGGAGCAACCACTCCGCAG	256
Db	144	TGGCCCTCCATCCAGAAACCTATGACCTACCCGCTACTCTGGAGCAACCACTCCGCAG	203
QY	257	CTTGGCTGGGACCTATCTGAATACCTCTGGGCCCCCTTTCAACGAGCAGACTTCAACCC	316
Db	204	CTTGGCTGGGACCTATCTGAATACCTCTGGGCCCCCTTTCAACGAGCAGACTTCAACCC	263
QY	317	TCCCGGCTGGGACAGACTCTGCCAGGGCCACTTGTGACTTGGAGTGTGGGAAG	376
Db	264	TCCCGGCTGGGACAGACTCTGCCAGGGCCACTTGTGACTTGGAGTGTGGGAAG	323
QY	377	CCTCAATGACAACTGGGGGTGACCCAGAACTACGAGGCTTACAGCCACTTCTGTGTTA	436
Db	324	CCTCAATGACAACTGGGGGTGACCCAGAACTACGAGGCTTACAGCCACTTCTGTGTTA	383
QY	437	CTTGGCTGGGCTCAACCGTACGGTGCACCTGTGAGCTGGGGGAGCTTGGCCACTT	496
Db	384	CTTGGCTGGGCTCAACCGTACGGTGCACCTGTGAGCTGGGGGAGCTTGGCCACTT	443
QY	497	CTGACACAGCTCCAGGGCTCTGGGCGCATTTGGGGGCTCATGSCAGCTCTGGGCTA	556
Db	444	CTGACACAGCTCCAGGGCTCTGGGCGCATTTGGGGGCTCATGSCAGCTCTGGGCTA	503
QY	557	CCCACTGCCAGCGCTGGGACTGAACCCACTTGGACTCTCTGGCCCTGCCACAG	616
Db	504	CCCACTGCCAGCGCTGGGACTGAACCCACTTGGACTCTCTGGCCCTGCCACAG	563
QY	617	TGACTTCTCCAGAGATGAGAGACTTCTGGCTCTGAAGAGCTGAGACCTGGCTGTG	676
Db	564	TGACTTCTCCAGAGATGAGAGACTTCTGGCTCTGAAGAGCTGAGACCTGGCTGTG	623
QY	677	GGCTCGGCCCAAGAGACTTCAACCGGCTCAAGAAGAGATGACGCTCCAGCAGCTGCAGT	736
Db	624	GGCTCGGCCCAAGAGACTTCAACCGGCTCAAGAAGAGATGACGCTCCAGCAGCTGCAGT	683
QY	737	CACCTGACACTGGGGCTCATGCTTCTGACTTCTGACCTTCTCCTTTCGCTCCCC	794
Db	684	CACCTGACACTGGGGCTCATGCTTCTGACTTCTGACCTTCTCCTTTCGCTCCCC	741
RESULT 3			
LOCUS	CK130210		
DEFINITION	AGENCOURT 15196910 NIH MGC 195 Homo sapiens cDNA clone	linear	EST 02-DEC-2003
ACCESSION	IMAGE:7002178 5', mRNA sequence.		
VERSION	CK130210		
KEYWORDS	EST.		
SOURCE	CK130210.1 GI:38622146		
ORGANISM	Homo sapiens (human)		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
JOURNAL	NTH-MGC http://mgi.nci.nih.gov/ .		
COMMENT	1 (bases 1 to 787)		
	National Institutes of Health, Mammalian Gene Collection (MGC)		
	Unpublished (1999)		
	Contact: Daniela S. Gerhard, Ph.D.		
	Office of Cancer Genomics		
	National Cancer Institute / NIH		
	Bldg. 31 Rm10A07 Bethesda, MD 20892		
	Email: cgabbe-remail.nih.gov		
	Tissue Procurement: Narayan Bhat		
	cDNA Library Preparation: Bhat Laboratory		
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)		
	DNA Sequencing by: Agencourt Bioscience Corporation		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LLNL at:		
	http://image.llnl.gov		
	Plate: IRBK4 row: e column: 08		
	High quality sequence stop: 715.		

FEATURES

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/clone_lib="NIH MGC 195"
/note="Vector: pDNR-Dual; Site 1: loxp-SalI; Site 2: loxp-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxp sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
a Note: this is a NIH_MGC Library."

ORIGIN

Query Match 88.7%; Score 706.8; DB 14; Length 787;
Best Local Similarity 99.4%; Pred No. 6e-136; Indels 0; Gaps 0;
Matches 708; Conservative 0; Mismatches 4;
84 AGCCCCATGGACCTCCGAGCAGGGGACTGTGGGGGATGTTAGCTGTGCTGTGACGGTG 143
Db 1 AGCCCCATGGACCTCCGAGCAGGGGACTGTGGGGGATGTTAGCTGTGCTGTGACGGTG 60
QY 144 CTCTGGCCTCCCTCGACGTGCGCAGTCTCAATCCAGAGGAGCCAGGGGCTGGCCCC 203
Db 61 CTCTGGCCTCCCTCGACGTGCGCAGTCTCAATCCAGAGGAGCCAGGGGCTGGCCCC 120
QY 204 TCCATCCAGAAACCTATGACCTCACCGCTACCTGGAGCACCACCTCCGAGCTTGGCT 263
Db 121 TCCATCCAGAAACCTATGACCTCACCGCTACCTGGAGCACCACCTCCGAGCTTGGCT 180
QY 264 GGGACCTATCTGAACCTACTGGGGCCCCCTTTCAAGAGCAGACTTCAACCTCCCGCC 323
Db 181 GGGACCTATCTGAACCTACTGGGGCCCCCTTTCAAGAGCAGACTTCAACCTCCCGCC 240
QY 324 CTGGGGGAGAGACTCTGCCAGGGCCACTGTGTGACTTGGAGGTGGCGAAGCTCAAT 383
Db 241 CTGGGGGAGAGACTCTGCCAGGGCCACTGTGTGACTTGGAGGTGGCGAAGCTCAAT 300
QY 384 GACAACTGGGCTGACCCAGAACTACAGGGCTTACAGCCACTTCTGTGTACTTGGCT 443
Db 301 GACAACTGGGCTGACCCAGAACTACAGGGCTTACAGGGCTTCTGTGTACTTGGCT 360
QY 444 GGCCTCAACCGTCAGCTGCGCAGTCTGAGTGGCGCGCAGCTGCGCCACTTCTGCAAC 503
Db 361 GGCCTCAACCGTCAGCTGCGCAGTCTGAGTGGCGCGCAGCTGCGCCACTTCTGCAAC 420
QY 504 AGCTTCCAGGGGCTCTGGGCGAGCAATTCGGGCGCTCATGGCAGCTCTGGGCTTACCACT 563
Db 421 AGCTTCCAGGGGCTCTGGGCGAGCAATTCGGGCGCTCATGGCAGCTCTGGGCTTACCACT 480
QY 564 CCGGAGCGCTGCTGGGAGCTGAAACCCACTTGGACTCTGGCCCTGCCAGCAGTACTTC 623
Db 481 CCGGAGCGCTGCTGGGAGCTGAAACCCACTTGGACTCTGGCCCTGCCAGCAGTACTTC 540
QY 624 CTCCAGAGATGAGCAGACTTCTGGCTGTGAAGAGCTGCGAGACTTGGCTGTGGGCTCG 683
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QY 684 GCCAAGGACTTCAACCGGCTCAAGAGAGATGAGAGCTTCCAGAGCTGCGAGTCAACCTG 743

clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: IRBK4 row: e column: 09

High quality sequence start: 13

High quality sequence stop: 711.

FEATURES

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/note="vector: pDNR-Dual; Site 1: loxP-Sall; Site 2: loxP-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxP sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearrayed_plates/IRBK.presv.dat
a Note: this is a NIH_MGC Library."

Query Match 87.7%; Score 698.6; DB 14; Length 804;
Best Local Similarity 99.2%; Pred. No. 3e-134;
Matches 712; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

Qy 77 CAGCCCCGACCTCGAGCAGGGGACTGTGGGGATTTAGCGCTGTG 136
Db |||||
25 CAGTCGACGCCATGACCTCCGAGCAGGGGACTGTGGGGATTTAGCGCTGTG 84
Qy 137 CAGGTGCTCTGGACCTCCTCGAGTCCAGTCTCAATCGCACAGGGGACCCAGGGCC 196
Db |||||
85 CAGGTGCTCTGGACCTCCTCGAGTCCAGTCTCAATCGCACAGGGGACCCAGGGCC 144
Qy 197 TGGCCCTCCATCCAGAAAACCTATGACCTCACCGCTACTCGAGCACCACTCCGGCAG 256
Db |||||
145 TGGCCCTCCATCCAGAAAACCTATGACCTCACCGCTACTCGAGCACCACTCCGGCAG 204
Qy 257 CTTGGCTGGACCTATCTGAACCTCTGGGCCCCCTTTCAACGAGCCAGACTTCAACCC 316
Db |||||
205 CTTGGCTGGACCTATCTGAACCTCTGGGCCCCCTTTCAACGAGCCAGACTTCAACCC 264
Qy 317 TCCCGCTGGGCGCAGACTCTGCCAGGGCCACTGTTGACTTGGAGTGTGGCGAAG 376
Db |||||
265 TCCCGCTGGGCGCAGACTCTGCCAGGGCCACTGTTGACTTGGAGTGTGGCGAAG 324
Qy 377 CTTCAATGACAACTGCGGTGACCCAGAACTACGAGGCTTACAGCACTTCTGTGTTA 436
Db |||||
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Qy 437 CTTGCGTGGCTCAACCGTCCAGGTCCTGCTGAGCTGCGCGGAGCTGGCCCACTT 496
Db |||||
385 CTTGCGTGGCTCAACCGTCCAGGTCCTGCTGAGCTGCGCGGAGCTGGCCCACTT 444
Qy 497 CTGCACCAAGCTCCAGGGCTGTGGGAGCACTTGGGGGCTCATGGCAGCTCTGGGGCTA 556
Db |||||
445 CTGCACCAAGCTCCAGGGCTGTGGGAGCACTTGGGGGCTCATGGCAGCTCTGGGGCTA 504
Qy 557 CCACACTGCCAGCGCTGCTGGGAGTGAACCCACTTGAACCTTGGCCCTGCCCCACAG 616
Db |||||
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ORIGIN

RESULT 6
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DEFINITION AGENCOURT_15197006 NIH_MGC 195 Homo sapiens cDNA clone
IMAGE:7002181 5', mRNA sequence.
CF271925
ACCESSION CF271925
VERSION CF271925.2 GI:38558833
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 752)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT On Aug 12, 2003 this sequence version replaced gi:33627837.
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: Bhat Laboratory
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: IRBK4 row: e column: 11
High quality sequence stop: 743.
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/clone_lib="NIH_MGC 195"
/note="vector: pDNR-Dual; Site 1: loxP-Sall; Site 2: loxP-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxP sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearrayed_plates/IRBK.presv.dat
a Note: this is a NIH_MGC Library."

ORIGIN

Qy 617 TGACTTCTCCAGAGATGGAGCACTTCTGGTGTGAGGAGCTGCAGACTGCTGTG 676
Db |||||
565 TGACTTCTCCAGAGATGGAGCACTTCTGGTGTGAGGAGCTGCAGACTGCTGTG 624
Qy 677 GGGCTCGGCCAAGGACTTCAACCGGCTCAAGAGAGATGCAGCTCCAGCAGCTGCAGT 736
Db |||||
625 GGGCTCGGCCAAGGACTTCAACCGGCTCAAGAGAGATGCAGCTCCAGCAGCTGCAGT 684
Qy 737 CACCTTGACCTGGGGCTCATGGCTTCTGACTTCTGACCTTCTCTCTTGGCTCCCC 794
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Db      445 TGCACCGCTCCAGGGCGCTGCTGGGAGCATTGGGGCGTCATGGGAGCTCTGGGCTAC 504
QY      558 CCACTGCCCCAGCGCTCCCTGGAGCTGAACCCACTTGGACTCTCTGGCCCTGCCACAGT 617
Db      505 CCACTGCCCCAGCGCTCCCTGGAGCTGAACCCACTTGGACTCTCTGGCCCTGCCACAGT 564
QY      618 GACTTCTCCAGAGATGAGAGCTTCTGGCTGTGCTGAAGAGCTGCAGACTGGCTGTGG 677
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LOCUS   AY409170
DEFINITION Homo sapiens HCM3468 gene, VIRTUAL TRANSCRIPT, partial sequence,
Genomic survey sequence.
ACCESSION AY409170
VERSION   AY409170.1 GI:39765138
KEYWORDS GSS.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
          1 (bases 1 to 662)
          Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
          Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
          Ferrera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
          Adams,M.D. and Cargill,M.
          Adams,M.D. and Cargill,M.
          Inferring nonneutral evolution from human-chimp-mouse orthologous
          gene trios
          Science 302 (5652), 1960-1963 (2003)
          14671302
REFERENCE 2 (bases 1 to 662)
AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
          Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
          Ferrera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
          Adams,M.D. and Cargill,M.
          Adams,M.D. and Cargill,M.
          Direct Submission
          Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
          Rockville, MD 20850, USA
          This sequence was made by sequencing genomic exons and ordering
          them based on alignment.
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    Best Local Similarity 100.0%; Pred. No. 1e-126;
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QY      106 GGGACTGTGGGGATGTAGCTGCTGTGCAGCGTCTGTGCACCTCCCTGCGAGTGC 165
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Db      121 TCACCCGCTACCTGGAGCACCAACTCCGAGCTTGGCTGGGACCTATCTGAACCTACTG 180
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Db      181 GCCCCCTTTTCAACGAGCCAGACTTCAACCCCTCCCGCTGGGGGAGAGACTCTGCCCA 240
QY      346 GGGCCACTTGTGACTTGGAGGTGTGGCGAAGCTTCAATGACAACTCGCGGTGACCCAGA 405
Db      241 GGGCCACTTGTGACTTGGAGGTGTGGCGAAGCTTCAATGACAACTCGCGGTGACCCAGA 300
QY      406 ACTACGAGCGCTACAGCCACCTTCTGTGTACTTGGTGGCTCAACCCCTCAGGCTGCCA 465
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QY      586 AACCCACTTGGACTCTCTGGCCCTGGCCCACTGAGTCTTCCAGAGATGAGACGACTTCT 645
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Db      541 GGCTGCTGAAGAGCTGCAGACTGGCTGGGCTCGGCGCAAGGACTTCAACCGCTCA 600
QY      706 AGAAGAAGATGAGCGCTCCAGCAGCTGCAGTCAACCTGCACCTGGGGCTCATGGCTTCT 765
Db      601 AGAAGAAGATGAGCGCTCCAGCAGCTGCAGTCAACCTGCACCTGGGGCTCATGGCTTCT 660
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Db      661 GA 662

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DEFINITION AGENCOURT_8864294 Lupski_sciatic_nerve Homo sapiens cDNA clone
IMAGE:6197786 5', mRNA sequence.
ACCESSION BQ940483
VERSION   BQ940483.1 GI:22355961
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
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          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
          1 (bases 1 to 1157)
          NIH-MGC http://mgs.nci.nih.gov/.
          National Institutes of Health, Mammalian Gene Collection (MGC)
          Unpublished (1999)
          Contact: Robert Strausberg, Ph.D.
          Email: cgapbs@mail.nih.gov
          Tissue Procurement: Dr. James R. Lupski
          cDNA Library Preparation: Life Technologies, Inc.
          DNA Sequencing Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          Cloned by: Agencourt Bioscience Corporation
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: LLAM13608 row: g column: 03
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/tissue_type="sciatic nerve"
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Directionally cloned using the following adaptors:
5'-TCGACCCAGCGCTCG-3' and
5'-GACTAGTTCTAGATCGGAGCGCGCCT(15)-3'. Size selected >
1 kb for average insert length 1.87 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
College of Medicine) and is available through Life
Technologies."

ORIGIN
Query Match      82.4%; Score 656.4; DB 13; Length 1157;
Best Local Similarity 97.4%; Pred. No. 1.9e-125;
Matches 678; Conservative 0; Mismatches 16; Indels 2; Gaps 1;

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DB 58 AGGGGACTCGTGGGGATGTTAGCGTGTGTCACGGTGTCTGGCACCTCCCTCGCAGT 117
QY 164 GCAGCTCTCAATCGCACAGGGGACCCAGGGCTGGCCCTCCATCCAGAAACCTATGA 223
DB 118 GCAGCTCTCAATCGCACAGGGGACCCAGGGCTGGCCCTCCATCCAGAAACCTATGA 177
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DB 178 CTTACCCCTCTACCTGGAGCACCACTCCGAGCTTGGCTGGGACTATCTGAATACCT 237
QY 284 GGGCCCCCTTTCAAGAGCCAGACTTCAACCTCCCGCTGGGGGAGAGACTCTGCC 343
DB 238 GGGCCCCCTTTCAAGAGCCAGACTTCAACCTCCCGCTGGGGGAGAGACTCTGCC 297
QY 344 CAGGGCACTGTGACTTGGAGGTGGGAGAGCTCAATGACAACTCGGCTGACCCA 403
DB 298 CAGGGCACTGTGACTTGGAGGTGGGAGAGCTCAATGACAACTCGGCTGACCCA 357
QY 404 GAATACGAGGCTTACAGCCACTTCTGTGTACTTGGTGGCTCAACCGTCAAGCTGC 463
DB 358 GAATACGAGGCTTACAGCCACTTCTGTGTACTTGGTGGCTCAACCGTCAAGCTGC 417
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DB 418 CACTGTGAGCTGGCGGAGCTGGCCACTTCTGCAACGAGCTCCAGGCGCTCTGGG 477
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DB 478 CAGATTGGGGGCTCATGGAGCTCTGGGCTACCCACTTGGCCCGCCGCTGCTGGGAC 537
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QY 644 CTGGCTGTGAAGAGCTGCAGAGCTGTGGCTGTGGCTCGGCAAGAGACTTCAACCGGCT 703
DB 598 CTGGCTGTGAAGAGCTGCAGAGCTGTGGCTGTGGCTCGGCAAGAGACTTCAACCGGCT 657
QY 704 CAAGAAGAGATGACGCTCCAGAGCTGAGTACCTTGCACCTTGGGGG--CTCATGGC 761
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DB 718 TTCTGACTTGTGACCTTCTCTCTTCTGCTCCCGCCC 753

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RESULT 10
AY409171
LOCUS      Pan troglodytes HCN3468 gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION

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genomic survey sequence.
ACCESSION      AY409171
VERSION        AY409171.1 GI:39765139
KEYWORDS       GSS.
SOURCE         Pan troglodytes (chimpanzee)
ORGANISM       Pan troglodytes
REFERENCE      1 (bases 1 to 662)
AUTHORS        Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
                Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
                Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
                Adams, M.D. and Cargill, M.
                Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
                Rockville, MD 20850, USA
TITLE          Direct Submission
JOURNAL        This sequence was made by sequencing genomic exons and ordering
                them based on alignment.
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Query Match      82.1%; Score 654; DB 29; Length 662;
Best Local Similarity 99.2%; Pred. No. 4.7e-125;
Matches 657; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 106 GGGACTCGTGGGGATGTTAGCGTGTGTCACGGTGTCTGGCACCTCCCTCGCAGTGC 165
DB 1   GGGACTCGTGGGGATGTTAGCGTGTGTCACGGTGTCTGGCACCTCCCTCGCAGTGC 60
QY 166 CAGCTCTCAATCGCACAGGGGACCCAGGGCTGGCCCTCCATCCAGAAACCTATGACC 225
DB 61  CAGCTCTCAATCGCACAGGGGACCCAGGGCTGGCCCTCCATCCAGAAACCTATGACC 120
QY 226 TCACCCGCTACCTGGAGCATCAACTCCGAGCTTGGCTGGGACCTATCTGAATACCTGG 285
DB 121 TCACCCGCTACCTGGAGCATCAACTCCGAGCTTGGCTGGGACCTATCTGAATACCTGG 180
QY 286 GCCCCCTTTCAACAGCCAGCTTCAACCCCTCCCGCTGGGGGAGAGACTCTGCCCA 345
DB 181 GCCCCCTTTCAACAGCCAGCTTCAACCCCTCCCGCTGGGGGAGAGACTCTGCCCA 240
QY 346 GGGCACTGTGACTTGGAGGTGTGGAGAGCTCAATGACAAACTGGGCTGACCCAGA 405
DB 241 GGGCACTGTGACTTGGAGGTGTGGAGAGCTCAATGACAAACTGGGCTGACCCAGA 300
QY 406 ACTACGAGGCTTACAGCCACTTCTGTGTACTTGGTGGCCCTCAACCGTCAGGCTGCCA 465
DB 301 ACTACGAGGCTTACAGCCACTTCTGTGTACTTGGTGGCCCTCAACCGTCAGGCTGCCA 360
QY 466 CTGCTGAGCTGGCGCAGCTGGCCCACTTCTGCAACAGCTCCAGGGCTCTCTGGGCA 525
DB 361 CTGCTGAGCTGGCGCAGCTGGCCCACTTCTGCAACAGCTCCAGGGCTCTCTGGGCA 420
QY 526 GCATTGGGGGCTCATGGAGCTTGGGCTTACCCACTGCCCCAGCGCTCCCTGGGACTG 585
DB 421 GCATTGGGGGCTCATGGAGCTTGGGCTTACCCACTGCCCCAGCGCTCCCTGGGACTG 480
QY 586 AACCCACTTGGACTCTCTGGCCCTGCCACAGTGAATCTTCTCCAGAAAGATGAGCACTTCT 645

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481 AACCCACTTGGAGCTCTCGGCGCTGCCACAGTGAATCTCTCCAGAGATGAGGACTTCT 540
QY 646 GGCTGCTGAAGGAGCTGCAGACCTGGCTGGCGCTGGCCAGGAGCTTCAACCGGCTCA 705
Db 541 GGCTGCTGAAGGAGCTGCAGACCTGGCTGGCGCTGGCCAGGAGCTTCAACCGGCTCA 600
QY 706 AGAAGAAGATGCAGCTCCAGAGCTGCAGCTCACTCCCTGCACCTGGGGGCTCATGGCTTCT 765
Db 601 AGAAGAAGATGCAGCTCCAGAGCTGCAGCTCACTCCCTGCACCTGGGGGCTCATGGCTTCT 660
QY 766 GA 767
Db 661 GA 662

RESULT 11
CF271926/c
LOCUS
DEFINITION AGENCOURT_15196988 NIH_MGC_195 Homo sapiens cDNA clone
IMAGE:7002180 5', mRNA sequence.
CF271926
ACCESSION CF271926.2 GI:38453379
VERSION
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 800)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT On Aug 12, 2003 this sequence version replaced gi:33627838.
Contact: Daniela S. Gerhardt, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgabs-re@mail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: Bhat Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: IRBK4 row: e column: 10
High quality sequence start: 8
High quality sequence stop: 720.
Location/Qualifiers
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/mol_type="mRNA"
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/note="Vector: pDNR-Dual; Site 1: loxP-Sall; Site 2:
loxP-HindIII; Clones from this library have been
PCR-amplified using gene-specific primers to contain the
complete open reading frame (based on known gene sequences
available from NCBI's RefSeq). Template for PCR is cDNA
derived from either pooled cytoplasmic polyA RNA from 30
cells lines or pooled total RNA from 10 different tissues
(from BD Biosciences/Clontech and Washington University).
PCR products are directionally cloned into the loxP sites
of the pDNR-Dual vector. Library constructed by Dr.
Narayan Bhat, Earl Bere III and Hongling Liao (Gene
Expression Laboratory, Research Technology Program, SAIC
Frederick, NCI-Frederick, Frederick, MD 21702). For
information on which gene each clone represents, please
visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearrayed_plates/IRBK.prsSV.dat

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a Note: this is a NIH_MGC Library."
ORIGIN
Query Match 81.2%; Score 647.2; DB 14; Length 800;
Best Local Similarity 99.2%; Pred. No. 1.3e-123;
Matches 660; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
QY 131 CTTGTGCACGGTGTCTCTGGCACCTCCCTGCAGTGCAGCTCTCAATGCGACAGGGGACCC 190
Db 753 CCCTTGCACGGTGTCTCT-GCACCTCCCTGCAGTGCAGCTCTCAATGCGACAGGGGACCC 695
QY 191 AGGGCTGGCCCTCCATCCAGAAAACCTATGACCTACCCGCTACCTGGAGCACAACCT 250
Db 694 AGGGCTGGCCCTCCATCCAGAAAACCTATGACCTACCCGCTACCTGGAGCACAACCT 635
QY 251 CCGCAGCTTGGCTGGGAGCTATCTCAACTACCTGGGGCCCCCTTTTCAACGAGCAGACTT 310
Db 634 CCGCAGCTTGGCTGGGAGCTATCTCAACTACCTGGGGCCCCCTTTTCAACGAGCAGACTT 575
QY 311 CAACCTTCCCGCTGGGGGCGAGACTCTGCCAGGCGCACTGTTGACTTGGAGGTGTG 370
Db 574 CAACCTTCCCGCTGGGGGCGAGACTCTGCCAGGCGCACTGTTGACTTGGAGGTGTG 515
QY 371 GCGAAGCTCTCAATGACAAACTGCGGCTGACCCAGAACTACGAGGCTACAGCCACTTCT 430
Db 514 GCGAAGCTCTCAATGACAAACTGCGGCTGACCCAGAACTACGAGGCTACAGCCACTTCT 455
QY 431 GTGTTACTTGGTGGCTCAACCGTCAAGGCTGCCACTGCTGAGTGCGCCGCGAGCTGCG 490
Db 454 GTGTTACTTGGTGGCTCAACCGTCAAGGCTGCCACTGCTGAGTGCGCCGCGAGCTGCG 395
QY 491 CCACCTTGCACAGGCTCCAGGCGCTGCTGGGAGCACTTGGGGGCTCATGGAGCTCT 550
Db 394 CCACCTTGCACAGGCTCCAGGCGCTGCTGGGAGCACTTGGGGGCTCATGGAGCTCT 335
QY 551 GGGCTACCCACTGCCCCCAGCGCTGCTGGGAGCTCAACCCACTTGGAGCTCTCTGGCCCTGC 610
Db 334 GGGCTACCCACTGCCCCCAGCGCTGCTGGGAGCTCAACCCACTTGGAGCTCTCTGGCCCTGC 275
QY 611 CCACAGTGAATCTCTCCAGAGATGAGACTTCTGGCTGCTGAAGGAGCTGCAGACCTG 670
Db 274 CCACAGTGAATCTCTCCAGAGATGAGACTTCTGGCTGCTGAAGGAGCTGCAGACCTG 215
QY 671 GCTGTGGGCTCGGCGCAAGGACTTCAACCGGCTCAAGAGAGAGATGCGAGCTCCAGCAGC 730
Db 214 GCTGTGGGCTCGGCGCAAGGACTTCAACCGGCTCAAGAGAGAGATGCGAGCTCCAGCAGC 155
QY 731 TCAGTCAACCTGCACTGGGGGCTCATGGCTTCTGACTTTCGACTTCTCTCTTGGCT 790
Db 154 TGCAGTCAACCTGCACTGGGGGCTCATGGCTTCTGACTTTCGACTTCTCTCTTGGCT 95
QY 791 CCCCC 795
Db 94 CCCCC 90

RESULT 12
BG437538
LOCUS
DEFINITION BG437538 853 bp mRNA linear EST 14-MAR-2001
mrna sequence.
ACCESSION BG437538
VERSION BG437538.1 GI:13344044
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 853)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.

```

Email: cgapbs@mail.nih.gov
 Tissue Procurement: DCTB/DTF/Gazdar
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLCMI384 row: i column: 19
 High quality sequence stop: 761.

FEATURES

source

1..853
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 /db_xref="taxon:9606"
 /clone="IMAGE:4621530"
 /tissue_type="large cell carcinoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC 18"
 /note="Organ: lung; Vector: pOTB7; Site: 1: XhoI; Site: 2:
 EcoRI; cDNA made by oligo-dr priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGCACGAG(G). Library constructed by Ling Hong in the
 laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
 NIH_MGC Library."

ORIGIN

Query Match 80.5%; Score 641.6; DB 12; Length 853;
 Best Local Similarity 96.9%; Pred. No. 2e-122;
 Matches 729; Conservative 0; Mismatches 14; Indels 9; Gaps 7;

QY 52 GGAGAGGACCCACCCCGCGCCAGCCCGCCAGCCCTGAGCTCCGACGAGGGACT 111
 DB 1 GGAGAGGACCCAGCCCGCGCCCGCCCGCCAGCCCTGAGCTCCGACGAGGGACT 60
 QY 112 CTTGGGGGATGTTAGCGTGCCTGTGACGGTGTCTGGCACCCTCCCTCAGTGCAGCTC 171
 DB 61 CTTGGGGGATGTTAGCGTGCCTGTGACGGTGTCTGGCACCCTCCCTCAGTGCAGCTC 120
 QY 172 TCAATGCGACAGGAGCCAGGCGCTGGCCCTCATCGAGAAACCTATGACCTACCC 231
 DB 121 TCAATGCGACAGGAGCCAGGCGCTGGCCCTCATCGAGAAACCTATGACCTACCC 180
 QY 232 GCTACTCGAGACCAACCTCCGAGCTTGGCTGGGACCTATCTGAACCTACCTGGGCCCCC 291
 DB 181 GCTACTCGAGACCAACCTCCGAGCTTGGCTGGGACCTATCTGAACCTACCTGGGCCCCC 240
 QY 292 CTTTCAACGAGCCAGACTTCAACCTCCCGCTGGGGGAGAGACTCTGCCCGAGGGCCA 351
 DB 241 CTTTCAACGAGCCAGACTTCAACCTCCCGCTGGGGGAGAGACTCTGCCCGAGGGCCA 300
 QY 352 CTTGTGACTTGAGGTGTCGCGAAGCTCAATGACAACTGGCGGTGACCCAGAACTACG 411
 DB 301 CTTGTGACTTGAGGTGTCGCGAAGCTCAATGACAACTGGCGGTGACCCAGAACTACG 360
 QY 412 AGCGCTACAGCCACCTTCTGTGTTACTGCTGGGCTCAACCGTCAGCTGCGACTGTGTG 471
 DB 361 AGCGCTACAGCCACCTTCTGTGTTACTGCTGGGCTCAACCGTCAGCTGCGACTGTGTG 420
 QY 472 AGCTGGCGCGACCTGGCCACTTCTGACACAGCTCCAGGCGCTGCTGGGCGAGATTG 531
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 QY 532 CGGGCGCTCATGGCAGCTCTGGGCTACCCAC-TGCCCGAGCGCTCCCTCGCTGGAC-TGAACC 589
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 QY 590 CACTTGGACTCTGGCCCTGCCACAGTACCTTCTCCAGAGATGGACGACTTCTGGCT 649
 DB 540 CACTTGGACTCTGGCCCTGCCACAGTACCTTCTCCAGAGATGGACGACTTCTGGCT 599

QY 650 GCTGAAGGAGCTGCACAGCTGGCTGTGGCGCTGGCCAGGAGACTTCAA-CCGGCTCAAGA 708
 DB 600 GCTGAAGGAGCTGAAGACCTGGCTGTGGCGCTGGCCAGGAGACTTCAAAGCCGGCTCAAGA 659
 QY 709 AGAAGATGACGCTCCAG-CAGCTGCAGTCAACCC---TGCACTGGGGGCTCATGGCTTC 764
 DB 660 AGAAGATGACGCTCCAGCCACCTGCAGTCAACCCCATGCACCTTGGAGGCTCATGGGTT 719
 QY 765 TGACTTCTGACC-TTCTCTCTTCGCTCCGCC 795
 DB 720 TGACTTCTGACCTTCTCTCTTCGCTCCGCC 751

RESULT 13

EG164929

LOCUS

DEFINITION

ACCESSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

EG164929 1053 bp mRNA linear EST 06-FEB-2001
 602343555F1 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:4453813 5',
 mRNA sequence.

EG164929 1 GI:12671563
 EST.
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1053)
 NIH-MGC <http://mgs.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
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 High quality sequence start: 3
 High quality sequence stop: 675.

FEATURES

source

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 /clone_lib="NIH MGC_89"
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 Site: 2: SalI; Cloned unidirectionally; oligo-dr primed.
 Average insert size 1.3 kb. Library enriched for
 full-length clones and constructed by Life Technologies.
 Note: this is a NIH_MGC Library."

ORIGIN

Query Match 77.9%; Score 621; DB 12; Length 1053;
 Best Local Similarity 94.1%; Pred. No. 3.9e-118;
 Matches 722; Conservative 0; Mismatches 35; Indels 10; Gaps 7;

QY 20 CGCGGCTCGCCCTCCACCTCCGCGAGGAGCGCCAGCCCGCGGCGCCAG 79
 DB 2 CGCGGCTCGCCCTCCACCTCCGCGAGGAGCGCCAGCCCGCGGCGCCAG 61
 QY 80 CCCAG-CCCATGAGACCTCCGAGAGAGGAGACTCTGTTGGGGGATGTTAGCTGCTGCA 138
 DB 62 CCCAGTCCCATGAGACCTCCGAGAGGAGGACTCTGTTGGGGGATGTTAGCTGCTGCA 121
 QY 139 CGTGTCTTGGCAGCTTCCCTGAGTGCAGCTTCAATCGCACAGGGGACCCAGGGCCCTG 198
 DB 122 CGTGTCTTGGCAGCTTCCCTGAGTGCAGCTTCAATCGCACAGGGGACCCAGGGCCCTG 181

QY 199 GCCCTCCATCCAGAAACCTATGACCTACCCCTACCTGGAGCAACAACTCCGAGCT 259
 Db 182 GCCCTCCATCCAGAAACCTATGACCTACCCCTACCTGGAGCAACAACTCCGAGCT 241
 QY 259 TGGCTGGAGCACTATGACCTACCTGGGCCCCC---TTTCAACGAGCCAGACTTCAAC 314
 Db 242 TGGCTGGAGCACTATGACCTAGCTTGGGCCCCCCTTTCACTAGACCTTCAAC 301
 QY 315 CTTCCCGCTGGGGGAGAGACTCTG-CCAGGGCCACTGTTCACTTGGAGTGTGGCG 373
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 QY 374 AAGCTCAATGACAACTCGGCTGACCCAGAACTAGAGCCCTACAGCACTTCTGTG 433
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 QY 434 TTACTTGGTGGCTCAACCGCTCAGGCTGACCTGCTGAGTGGCGCCGAGCTGGGCCA 493
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 QY 494 CTTCTGACAGCTCGAGGCTGCTGGGAGCACTTGGGGCGCTCATGGCAGCTTGGG 553
 Db 482 CTTCTGACAGCTCGAGGCTGCTGGGAGCACTTGGGGCGCTCATGGCAGCTTGGG 541
 QY 554 CTACCCACTG-CCCCAGCGCTGCTGGGAGCTGAACCCAC-TTGGACTCTGGCCCTGCC 611
 Db 542 CTACCCACTGCCCCAGCGCTGCTGGGAGCTGAACCCACTTGGACTCTGGCCCTGCC 601
 QY 612 CACAGTACTCTCCAGAGATGAGCACTTCTGGCTGCTGAAGAGCTGCAGACTGG 671
 Db 602 CACAGTACTCTCCAGAGATGAGCACTTCTGGCTGCTGAAGAGCTGCAGACTGG 661
 QY 672 CTGTGGGCTCGGCCAGAGCTTCAACCGGCTCAAGAGAGATGAGCCCTCCAGAGCT 731
 Db 662 CTGTGGGCTCGGCC-AGGACTTCCACCGTCCAGAGAGATGAGCCCTCCAGAGCT 720
 QY 732 GCAGTCACTGACCTGGGGGCTCATGGCTTCTGACTTCTGACTT 778
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RESULT 14
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 DEFINITION AGNC0015196924 NIH MGC 195 Homo sapiens cDNA clone
 IMAGE:7002178 5', mRNA sequence.
 ACCESSION CF271930
 VERSION CF271930.2 GI:38453381
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 801)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 On Aug 12, 2003 this sequence version replaced gi:33627842.
 Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: Narayan Bhat
 cDNA Library Preparation: Bhat Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
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 High quality sequence stop: 646.

FEATURES
source

Location/Qualifiers
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/note="Vector: pDNR-Dual; Site 1: loxp-SalI; Site 2: loxp-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxp sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBK.presv.dat
 A Note: this is a NIH_MGC Library."

ORIGIN

Query Match 75.9%; Score 604.8; DB 14; Length 801;
 Best Local Similarity 99.2%; Pred. No. 7.9e-115;
 Matches 606; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 185 GACCCAGGGCTGGCCCTCCATCCAGAAACCTATGACCTACCCGCTACCTGGAGCA 244
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 QY 245 CCAACTCCGAGCTTGGCTGGGACCTATCTGAACCTACCTGGGCCCCCTTTCAACAGGCC 304
 Db 642 CCAACTCCGAGCTTGGCTGGGACCTATCTGAACCTACCTGGGCCCCCTTTCAACAGGCC 583
 QY 305 AGACTTCAACCTCCCGCTGGGGGAGAGACTCTGCCAGGGGCACTGTGTGACTTGA 364
 Db 582 AGACTTCAACCTCCCGCTGGGGGAGAGACTCTGCCAGGGGCACTGTGTGACTTGA 523
 QY 365 GGTGTGGCGAAGCCCAATGACAACTCGGCTGACCCAGCACTAGAGGCTACAGCCA 424
 Db 522 GGTGTGGCGAAGCCCAATGACAACTCGGCTGACCCAGCACTAGAGGCTACAGCCA 463
 QY 425 CCTTCTGTGTTACTTGGTGGGCTCAACCGTCAGGCTGCCTGCTGAGCTGCGCGCAG 484
 Db 462 CCTTCTGTGTTACTTGGTGGGCTCAACCGTCGGGCTGCCTGCTGAGCTGCGCGCAG 403
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 QY 725 AGCAGGTGAGTCAACCTGACCTGGGGGCTCATGGCTTCTGACTTCTGACCTTCTCCTC 784
 Db 162 AGCAGGTGAGTCAACCTGACCTGGGGGCTCATGGCTTCTGACTTCTGACCTTCTCCTC 103
 QY 785 TTCGCTCCCCC 795

Db 102 TTCGCTCCCC 92

|||||

CF271924 763 bp mRNA linear EST 19-NOV-2003
AGENCY: 15197020 NIH MGC 195 Homo sapiens cDNA clone
IMAGE: 7002181 5', mRNA sequence.

CF271924
CF271924.2 GI:38453378
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NIH-MGC <http://mgs.nci.nih.gov/>
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
On Aug 12, 2003 this sequence version replaced gi:33627836.
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgabps@mail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: Bhat Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: IRBK4 row: e column: 11
High quality sequence start: 7
High quality sequence stop: 648.

FEATURES
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/clone_lib="NIH MGC 195"
/notes="Vector: pDNR-Dual; Site 1: loxp-SalI; Site 2:
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PCR-amplified using gene-specific primers to contain the
complete open reading frame (based on known gene sequences
available from NCBI's RefSeq). Template for PCR is cDNA
derived from either pooled cytoplasmic polyA RNA from 30
cells lines or pooled total RNA from 10 different tissues
(from BD Biosciences/Clontech and Washington University).
PCR products are directionally cloned into the loxp sites
of the pDNR-Dual vector. Library constructed by Dr.
Narayan Bhat, Earl Bere III and Hongling Liao (Gene
Expression Laboratory, Research Technology Program, SAIC
Frederick, NCI-Frederick, Frederick, MD 21702). For
information on which gene each clone represents, please
visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearrayed_plates/IRBK.presv.dat
a Note: this is a NIH_MGC Library."

Search completed: August 16, 2004, 04:01:32
Job time : 1823.54 secs

ORIGIN

Query Match 75.5%; Score 602; DB 14; Length 763;
Best Local Similarity 98.9%; Pred. No. 2.9e-114;
Matches 617; Conservative 0; Mismatches 5; Indels 2; Gaps 1;

Qy 172 TCAATCGCAGGGGACCCAGGCGCTGGCCCTCCATCCAGAAACCTATGACCTCAGCC 231
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Db 713 TCAATCGCAGGGG--CCAGGCGCTGGCCCTCCATCCAGAAACCTATGACCTCAGCC 656
|||||

Qy 232 GCTACCTGGAGCACCACCACTCCGAGCTTGGCTGGGACCTATCTGAACCTACCTGGGCCCCC 291
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 15, 2004, 12:15:49 ; Search time 272.88 Seconds
(without alignments)
12407.700 Million cell updates/sec

Title: US-09-931-704-1

Perfect score: 797
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Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 2: geneseqn1990s.*
- 3: geneseqn2000s.*
- 4: geneseqn2001as.*
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- 9: geneseqn2003cs.*
- 10: geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	797	100.0	797	2	AAV22652 cDNA enco
2	797	100.0	797	2	AAV47510 Human neu
3	797	100.0	797	3	AAV39481 Human NNT
4	797	100.0	797	6	ABK11647 Human CDN
5	793.4	99.5	881	4	AAH74484 Nucleotid
6	793.4	99.5	1790	3	AAA88546 Human int
7	759.2	95.3	768	4	AAH99772 Human pro
8	749.4	94.0	1710	2	AAH16161 Human car
9	710	89.1	729	4	AAD04201 Human car
10	694.8	87.2	1008	4	AAK51548 Human pol
11	689.4	84.0	819	2	AAV22654 cDNA enco
12	669.4	84.0	819	2	AAV47512 Mouse neu
13	669.4	84.0	819	3	AAA39483 Murine NN
14	669.4	84.0	819	6	ABK11649 Mouse CDN
15	668.4	83.9	968	4	ABA09140 Human car
16	668.4	83.9	968	4	AAK52532 Human pol
17	558.4	70.1	648	3	AAA88547 Human int
18	523.4	65.7	5087	3	AAA39482 Human NNT
19	523.4	65.7	5087	6	ABK11648 Human nov
20	523.4	65.7	5088	2	AAV22653 Human gen
21	523.4	65.7	5088	2	AAV47511 Human neu
22	493.4	61.9	495	4	AAI25564 Probe #15
23	493.4	61.9	495	4	ABA71773 Human foe

C 24	493.4	61.9	495	4	AAI52108	AAI52108 Probe #20
C 25	493.4	61.9	495	4	ABA37855	ABA37855 Probe #16
C 26	493.4	61.9	495	4	AAK46202	AAK46202 Human bon
C 27	493.4	61.9	495	4	AAK20142	AAK20142 Human bra
C 28	493.4	61.9	495	4	ABS45921	ABS45921 Human liv
C 29	493.4	61.9	495	6	ABS20513	ABS20513 Human gen
C 30	369	46.3	492	4	AAI16384	AAI16384 Probe #63
C 31	369	46.3	492	4	ABA59256	ABA59256 Human foe
C 32	369	46.3	492	4	AAI39047	AAI39047 Probe #77
C 33	369	46.3	492	4	ABA27996	ABA27996 Probe #64
C 34	369	46.3	492	4	AAK33253	AAK33253 Human bon
C 35	369	46.3	492	4	AAK07469	AAK07469 Human bon
C 36	369	46.3	492	4	ABS33003	ABS33003 Human liv
C 37	369	46.3	492	6	ABS08085	ABS08085 Human gen
C 38	269.4	33.8	283	4	AAH23145	AAH23145 Osteoearth
C 39	80.2	10.1	396	2	AAH16162	AAH16162 Human ear
C 40	73.6	9.2	1260	6	ABQ16903	ABQ16903 Oligonucl
C 41	73.6	9.2	1260	6	ABQ16902	ABQ16902 Oligonucl
C 42	58.6	7.4	65	6	ABN56698	ABN56698 Mouse spl
C 43	49	6.1	627	2	AAK60797	AAK60797 Human DNA
C 44	46.8	5.9	1260	6	ABQ16904	ABQ16904 Oligonucl
C 45	46.8	5.9	1260	6	ABQ16905	ABQ16905 Oligonucl

ALIGNMENTS

RESULT 1
AAV22652
ID AAV22652 standard; cDNA; 797 BP.
AC AAV22652;
XX AAV22652;
DT 13-JUL-1998 (first entry)
XX cDNA encoding human neurotrophic factor NNT-1.

XX Human; neurotrophic factor; NNT-1; growth; motor; sympathetic; neuron;
KW treatment; neurological disease; degeneration; Parkinson's disease;
KW amyotrophic lateral sclerosis; ALS; Alzheimer's disease; stroke; ss.

OS Homo sapiens.

XX Key Location/Qualifiers
FT CDS 90..767
FT sig_peptide /*tag= a
FT mat_peptide /*tag= b
FT /*tag= c

XX US5741772-A.

XX 21-APR-1998.

XX 03-FEB-1997; 97US-00792019.

XX 03-FEB-1997; 97US-00792019.

XX (AMGE-) AMGEN INC.

XX Chang M;

XX WPI; 1998-260526/23.

XX P-PSDB; AAW56141.

XX Neurotrophic factor NNT-1 polypeptide and related nucleic acids - useful

XX for stimulating growth of motor and sympathetic neurons.

XX Disclosure; Fig 1; 41pp; English.

XX The present sequence encodes a human neurotrophic factor, designated NNT-

1, which is capable of stimulating growth of motor or sympathetic

CC neurons. The NNT-1 protein is useful in the treatment of neurological
 CC diseases characterised by the degeneration and death of particular
 CC classes of neurons. These diseases specifically include Parkinson's
 CC disease, amyotrophic lateral sclerosis (ALS), Alzheimer's disease, stroke
 CC and various degenerative disorders affecting vision
 XX
 SQ Sequence 797 BP; 139 A; 297 C; 218 G; 143 T; 0 U; 0 Other;
 Query Match 100.0%; Score 797; DB 2; Length 797;
 Best Local Similarity 100.0%; Pred. No. 3.6e-176;
 Matches 797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 DB 601 CTGGCCCTGCCACAGTACTTCTCCAGAGTGAAGTCTTGGCTTGGTGAAGGAGC 660
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 DB 661 TGCAGACCTTGGTGTGGGCTCGGCCAGAGACTTCAACCGGCTCAAGAGAGATGCGAGC 720
 QY 721 CTCACAGCTGACGTACCTGACCTGGGGCTCATGGCTTCTGACTTCTGACCTTCT 780
 DB 721 CTCACAGCTGACGTACCTGACCTGGGGCTCATGGCTTCTGACTTCTGACCTTCT 780
 QY 781 CTTCTTTCGCTCCCGCC 797
 DB 781 CTTCTTTCGCTCCCGCC 797

RESULT 2
 AAV47510
 ID AAV47510 standard; cDNA; 797 BP.
 XX

AC AAV47510;
 XX 09-NOV-1998 (first entry)
 DT Human neurotrophic factor NNT-1 cDNA.
 DE
 DE
 XX NNT-1; neurotrophic factor; human; antiinflammatory; adjuvant;
 XX Alzheimer's disease; Parkinson's disease; Huntington's disease;
 XX amyotrophic lateral sclerosis; Charcot-Marie-Tooth syndrome;
 XX peripheral neuropathy; dystrophy; neural retina degeneration;
 XX common variable immunodeficiency; CVID; selective IgA deficiency;
 XX hypogammaglobulinaemia; X-linked agammaglobulinaemia; antiseptic;
 XX therapy; ss.
 XX Homo sapiens.
 XX
 XX Key Location/Qualifiers
 XX CDS 90..767
 XX /*tag= a
 XX sig_peptide 90..170
 XX /*tag= b
 XX mat_peptide 171..764
 XX /*tag= c
 XX
 XX WO9833922-A1.
 XX
 XX 06-AUG-1998.
 XX
 XX 02-FEB-1998; 98WO-US002363.
 XX
 XX 03-FEB-1997; 97US-00792019.
 XX
 XX 30-JAN-1998; 98US-00016534.
 XX
 XX (AMGE-) AMGEN INC.
 XX
 XX Chang M, Elliot GS, Senaldi G, Sarmiento U;
 XX WPI; 1998-437475/37.
 XX P-PSDB; AAW29715.
 XX
 XX Newly isolated nucleic acid encoding human or murine neurotrophic factor
 XX NNT-1 - useful for treatment of neurological and immunological diseases
 XX or inflammation, also as vaccine adjuvant.
 XX
 XX Claim 3; Fig 1; 120pp; English.
 XX
 XX This newly isolated human cDNA sequence (deposited at ATCC 98295) codes
 XX for a novel neurotrophic factor, designated NNT-1 (see AAW29715), that is
 XX a growth factor for neurons and for B or T cells. It was obtained from a
 XX T-cell lymphoma cDNA library by expressed sequence tag analysis on the
 XX basis of homology to CNTF. The isolated NNT-1 cDNA was used as probe to
 XX isolate NNT-1 genomic DNA (see AAV47511). Vectors containing the cDNA or
 XX genomic DNA and host cells are provided for use in the production of NNT-
 XX 1 polypeptides. These are used to treat: (i) neurological or
 XX immunological diseases, specifically Alzheimer's, Parkinson's or
 XX Huntington's diseases, amyotrophic lateral sclerosis, Charcot-Marie-Tooth
 XX syndrome, peripheral neuropathy, dystrophy and degeneration of the neural
 XX retina, or conditions characterised by T or B cell defects, e.g. common
 XX variable immunodeficiency (CVID), selective IgA deficiency,
 XX hypogammaglobulinaemia and X-linked agammaglobulinaemia (claimed), but
 XX many others disclosed; and (ii) inflammation. NNT-1 is also able to boost
 XX immunoreactivity and antibody production following vaccination, and,
 XX since it inhibits tumour necrosis factor production, it may also be
 XX useful for treating sepsis. NNT-1 nucleic acid fragments are also used as
 XX hybridisation probes in diagnostic assays. In addition, cells that have
 XX been engineered to express NNT-1 can be implanted, or nucleic acids are
 XX delivered in gene therapy vectors
 XX
 XX Sequence 797 BP; 139 A; 297 C; 218 G; 143 T; 0 U; 0 Other;
 XX
 XX Query Match 100.0%; Score 797; DB 2; Length 797;
 XX Best Local Similarity 100.0%; Pred. No. 3.6e-176;
 XX Matches 797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX	retinopathy; immune disorder; hematopoietic disorder; ss.
XX	
OS	Homo sapiens.
XX	
XX	
FH	Location/Qualifiers
FT	90. .767
FT	/*tag= a
FT	/product= "NNT-1"
XX	
XX	
PN	US6054294-A.
XX	
XX	
PD	25-APR-2000.
XX	
XX	12-DEC-1997; 97US-00988819.
PF	
XX	03-FEB-1997; 97US-00792019.
PR	
XX	(AMGE-) AMGEN INC.
PA	
XX	
XX	Chang M;
XX	
XX	
XX	WPI; 2000-338492/29.
DR	P-PSDB; AAY87813.
DR	
XX	
PT	New nucleic acids encoding neurotrophic factors useful for stimulating
PT	growth of motor or sympathetic neurons for treating neuron cell damage
XX	
PS	Claim 1a; Fig 1; 42pp; English.
XX	
XX	This invention describes a novel nucleic acid molecule (I) encoding a
CC	novel neurotrophic factor (NNT-1) (II) which has neurotropic, and
CC	neuroprotective, anticonvulsant, antiparkinsonian, antidiabetic and
CC	ophthalmological activity. (I) is useful for producing NNT-1 polypeptides
CC	which are useful for treating patients in whom various cells of the
CC	central, autonomic, or peripheral nervous system have degenerated and/or
CC	have been damaged by congenital disease, trauma, mechanical damage,
CC	surgery, stroke, ischemia, infection, metabolic disease, nutritional
CC	deficiency, malignancy and/or toxic agents. NNT-1 proteins are used to
CC	treat diseases like Alzheimer's, Parkinson's, amyotrophic lateral
CC	sclerosis, Charcot-Marie-Tooth syndrome, Huntington's disease, peripheral
CC	neuropathy induced by diabetes or other metabolic disorders, and/or
CC	dystrophies or degeneration of the neural retina such as retinitis
CC	pigmentosa, drug-induced retinopathies, stationary forms of night
CC	blindness, progressive cone-rod degeneration, immune disorders and
CC	hematopoietic disorders. (I) is effective in treating neurological
CC	conditions and promotes neuron regeneration. Neural functions are
CC	effectively restored in patients suffering from various neurological
CC	disorders. This sequence encodes the human NNT-1 protein described in the
CC	method of the invention
XX	
SQ	Sequence 797 BP; 139 A; 297 C; 218 G; 143 T; 0 U; 0 Other;

Query Match 100.0%; Score 797; DB 3; Length 797;
Best Local Similarity 100.0%; Pred. No. 3.6e-176;
Matches 797; Conservative 0; Mismatches 0; Indels 0; Gaps 0

[illegible]


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Qy 781 CCTTCTGGCTCCCGCC 797
Db 781 CCTTCTGGCTCCCGCC 797

```

RESULT 4

ABK11647
ID ABK11647 standard; cDNA; 797 BP.

XX AC ABK11647;

XX DT 05-JUN-2002 (first entry)

XX DE Human cDNA encoding novel neurotrophic factor NNT1.

XX Human; ss; gene; NNT1; neurotrophic factor; IgE-related disease;
KW Type I allergic disease; allergic rhinitis; eczema; dermatitis;
KW pollinosis; asthma; immune disease; cancer; arteriosclerosis;
KW vascular restenosis; rheumatoid arthritis; psoriatic arthritis;
KW inflammatory arthritis; osteoarthritis; inflammatory joint disease;
KW autoimmune disease; multiple sclerosis; lupus; diabetes; endometriosis;
KW inflammatory bowel disease; transplant rejection; reproductive disorder;
KW graft versus host disease; infertility; miscarriage; preterm labour.

XX OS Homo sapiens.

PH Key Location/Qualifiers
FT CDS 90..767
FT /*tag= a
FT /product= "NNT1"

XX WO200215977-A2.

XX PN 28-FEB-2002.

XX PF 17-AUG-2001; 2001WO-US025906.

XX XX 18-AUG-2000; 2000US-0226436P.

```

PR 16-AUG-2001; 2001US-00931704.
PA (AMGE-) AMGEN INC.
PI Senaldi G;
XX WPI; 2002-280867/32.
XX P-PSDB; AAU78176.
XX Treating Immunoglobulin E-related disease, modulating IgE levels in a
XX patient, preventing IgE-related disease and treating allergic diseases,
XX involves administering NNT-1 inhibitor to a patient.
XX Claim 2; Fig 1; 63pp; English.
XX The invention relates to treating Immunoglobulin E (IgE)-related disease,
XX modulating IgE levels in a patient, preventing an IgE-related disease,
XX and treating allergic diseases, comprising administering a
XX therapeutically effective amount of novel neurotrophic factor (NNT)-1
XX inhibitor to a patient. Also included are a method of diagnosing an IgE-
XX related disease or susceptibility to an IgE-related disease, by
XX determining the presence or amount of expression of an NNT1 polypeptide
XX encoded by a NNT1 nucleotide sequence, its fragment or naturally
XX occurring variant, and diagnosing an IgE-related disease or
XX susceptibility of an IgE-related disease based on the presence or amount
XX of expression of the polypeptide and a pharmaceutical composition for use
XX in treating IgE-related disease, comprising the NNT1 inhibitor. The NNT1
XX inhibitor is useful for preventing and treating IgE-related disease,
XX modulating IgE levels, and treating allergic diseases e.g. Type I
XX allergic disease, allergic rhinitis, eczema, dermatitis, pollinosis,
XX asthma, immune diseases and disorders, diseases involving abnormal cell
XX proliferation including cancer, arteriosclerosis and vascular restenosis,
XX diseases and conditions relating to dysfunction of immune system
XX including rheumatoid arthritis, psoriatic arthritis, inflammatory
XX arthritis, osteoarthritis, inflammatory joint disease, autoimmune
XX disease, multiple sclerosis, lupus, diabetes, inflammatory bowel disease,
XX transplant rejection, and graft versus host disease, and reproductive
XX diseases and disorders including infertility, miscarriage, preterm labour
XX and delivery, and endometriosis. The present sequence encodes human NNT1
XX
XX Sequence 797 BP; 139 A; 297 C; 218 G; 143 T; 0 U; 0 Other;

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Query Match 100.0%; Score 797; DB 6; Length 797;

Best Local Similarity 100.0%; Pred. No. 3.6e-176;

Matches 797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 CGCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
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RESULT 5
AAH74484
ID AAH74484 standard; DNA; 881 BP.
AC AAH74484;
XX
XX
DT 15-OCT-2001 (first entry)
XX
XX Nucleotide sequence of a human NNT-1 protein.

XX NNT-1; CLF-1; SCNTFRalpha; nervous system; neuron; nervous system;
KW neuro-muscular function; tumour; immune system; haematopoietic system;
KW reproductive system; liver; skeletal muscle; neurodegenerative disease;
KW amyotrophic lateral sclerosis; Parkinson's disease; Huntington's disease;
KW muscular mass; paralysis; cancer; obesity; fertility; endometriosis;
KW blastocyst implantation; thrombosis; retinal disease;
KW retinal pigment; ss.
XX Homo sapiens.
XX
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PH Key Location/Qualifiers
FT CDS 174..851
FT FT /*tag= a
FT FT /product= "NNT-1"
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XX W02001:55172-A2.
XX
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XX 02-AUG-2001.
XX
XX 26-JAN-2001; 2001WO-FR000253.
XX
XX 27-JAN-2000; 2000FR-00001035.
XX 12-OCT-2000; 2000FR-00013089.
XX
XX (FABR) FABRE MEDICAMENT SA PIERRE.
XX (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
XX
XX Elson G, Gauchat J, Plun-Favreau H, Chevalier S, Gascan H;
XX
XX WPI; 2001-488773/53.
XX P-PSDB; AAG63543.
XX
XX A complex comprising a NNT-1 protein and a CLF-1 and/or SCNTFRalpha

PT protein useful to treat neurodegenerative disease including Parkinson's
PT and Huntington's, obesity and cancer.
XX
PS Disclosure; Page 57-58; 67pp; French.
XX
CC The present sequence encodes a human NNT-1 protein. The specification
CC describes a complex comprising a NNT-1 protein and a CLF-1 and/or
CC SCNTFRalpha protein. The NNT-1/CLF-1 complex is used to modulate activity
CC of the SCNTFRalpha/gli30/LiFrbeta receptor complex, or to induce
CC phosphorylation of the tyrosine of gli30 and LiFrbeta, particularly where
CC cells expressing the receptor complex are in the central or peripheral
CC nervous system, in neurons implicated in neuro-muscular function or in
CC skeletal muscle. The complex or antibodies are also used to decrease the
CC survival, growth or proliferation of tumour cells or to facilitate the
CC proliferation and/or inhibit differentiation of cells stocks. The complex
CC is also used to modulate activity of the gli30/LiFrbeta receptor or cells
CC expressing that receptor, particularly those cells implicated in the
CC immune, haematopoietic, nervous or reproductive system, the liver or
CC skeletal muscle. Molecules of the invention may be used to prevent or
CC treat neurodegenerative diseases including amyotrophic lateral sclerosis,
CC Parkinson's and Huntington's disease, to repair or regenerate nervous or
CC muscular tissue or to maintain muscular mass in paralysis patients. They
CC may also be used to treat cancer, obesity and associated diseases, and to
CC improve fertility, particularly to avoid endometriosis and/or assist
CC blastocyst implantation, thrombosis, or retinal disease, particular
CC retinal pigmentosis
XX
SQ Sequence 881 BP; 158 A; 318 C; 246 G; 159 T; 0 U; 0 Other;

Query Match 99.5%; Score 793.4; DB 4; Length 881;
Best Local Similarity 99.9%; Pred. No. 2.6e-175;
Matches 794; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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DB 85 ATTAAGCTTCGCGGAGCGCGGCTCGCCCTCCACCTCCGCGACGCTCCGGAGAGGAG 144
QY 61 CCGCACCG 120
DB 145 CCGCACCG 204
QY 121 TGTAGCTGCTGTGCGAGCTGTGCTGCGACCTCCCTGCGAGTGCAGCTTCAATCGCA 180
DB 205 TGTAGCTGCTGTGCGAGCTGTGCTGCGACCTCCCTGCGAGTGCAGCTTCAATCGCA 264
QY 181 CAGGGGACCCAGGGGCTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240
DB 265 CAGGGGACCCAGGGGCTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 324
QY 241 AGCACCAACTCGCGAGCTTGGCTGGGAGCTATCTGAACCTACTGGGGCGCGCGCGCG 300
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DB 445 TGGAGGTGTGGCGAAGCCTCAATGACAAACTGGCGCTGACCCAGAACTACGAGGCGCTACA 504
QY 421 GCCACCTTCTGTGTACTTGGCTGGCTCAACCGTCAGGCTGCCACTGCTGAGCTGGGCC 480
DB 505 GCCACCTTCTGTGTACTTGGCTGGCTCAACCGTCAGGCTGCCACTGCTGAGCTGGGCC 564
QY 481 GCAGCCTGGCCACTTCTGACCAAGCCTCCAGGGCTGTCTGGGAGAGATTTGGGCGGTCA 540
DB 565 GCAGCCTGGCCACTTCTGACCAAGCCTCCAGGGCTGTCTGGGAGAGATTTGGGCGGTCA 624
QY 541 TGGGAGCTCTGGGCTACCCACTGCCAGCCAGCCGCTGCTGGGAGACTGAACCCACTTGAATC 600
DB 625 TGGGAGCTCTGGGCTACCCACTGCCAGCCAGCCGCTGCTGGGAGACTGAACCCACTTGAATC 684

601 CTGGCCCTGCCACAGTGTCTCTCCAGAGATGAGAGTCTTGGCTGCTGAAGGAGC 660
 685 CTGGCCCTGCCACAGTGTCTCTCCAGAGATGAGAGTCTTGGCTGCTGAAGGAGC 744
 661 TGCAGACCTGGCTGTGGGCTCGGCCAAGGACTTCAACCGGCTCAAGAAGAGATGAGC 720
 745 TGCAGACCTGGCTGTGGGCTCGGCCAAGGACTTCAACCGGCTCAAGAAGAGATGAGC 804
 721 CTCAGACCTGACGTCAACCTGACCTGGGGCTCATGGCTTCTGACCTTCT 780
 805 CTCAGACCTGACGTCAACCTGACCTGGGGCTCATGGCTTCTGACCTTCT 864
 781 CCTCTTCGCTCCCCC 795
 865 CCTCTTCGCTCCCCC 879

RESULT 6

AAA88546
 ID AAA88546 standard; DNA; 1790 BP.
 AC AAA88546;
 XX
 DT 22-JAN-2001 (first entry)
 XX
 DE Human interleukin-B60 (IL-B60) gene.
 XX
 KW Interleukin-B60; IL-B60; human; cytokine; chromosome 11;
 KW cytokine-like factor-1; haematopoietic; inflammation; antiinflammatory;
 KW autoimmune disease; therapy; ds.
 XX

OS Homo sapiens.

XX Key Location/Qualifiers

XX CDS 162..809

XX FT /*tag= a

XX FT sig_peptide 162..212

XX FT /*tag= b

XX FT mat_peptide 213..806

XX FT /*tag= c

XX WO200053631-A1.

XX PN 14-SEP-2000.

XX PD 09-MAR-2000; 2000WO-US006182.

XX PR 11-MAR-1999; 99US-00267901.

XX PA (SCHE) SCHERING CORP.

XX PI Oppmann B, Timans JC, Kastelein RA, Bazan JF;

XX DR WPI; 2000-587426/55.

XX DR P-PSDB; AAB19686.

XX PT Cytokine-like factor 1 (CLF-1) and interleukin (IL)-B60 complexes,
 PT polypeptides and nucleic acids useful in research, diagnosis and for
 PT treating inflammatory and autoimmune disorders.
 XX
 PS Claim 17; Page 15-16; 97pp; English.

XX The present sequence is that of DNA encoding human interleukin-B60 (IL-
 CC B60, see AAB19586), a novel, small soluble cytokine-like protein of 198
 CC amino acids that exhibits structural motifs characteristic of a member of
 CC the long-chain cytokines, and which shows homology to granulocyte colony
 CC stimulating factor and interleukin-6. IL-608 may have either stimulatory
 CC or inhibitory effects on haematopoietic cells, including e.g. lymphoid
 CC cells, such as T-cells, B-cells, natural killer cells, macrophages,
 CC dendritic cells, haematopoietic progenitors, etc. Methods are provided
 CC for modulating the physiology or development of a cell or tissue culture
 CC cells by contacting the cell with an agonist or antagonist of IL-B60 or
 CC an agonist of antagonist of a complex of mature IL-B60 and its partner.

CC cytokine-like factor-1 (CLF-1, see AAB19588). The IL-B60/CLF-1 cytokine
 CC serves as a key physiological factor in motor neuron development and
 CC regeneration. IL-60B, its agonists and antagonists may be used to treat
 CC inflammatory or autoimmune disorders and also for drug screening. The
 CC IL60B gene maps to human chromosome 11

XX Sequence 1790 BP; 381 A; 560 C; 474 G; 375 T; 0 U; 0 Other;

Query Match 99.5%; Score 793.4; DB 3; Length 1790;

Best Local Similarity 99.9%; Pred. No. 3e-175;

Matches 794; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATTTAAAGCTTGGCCGAGCGGGCTCGCCCTCCCACTCGGCAGGCTCGGGAGGAG 60

DB 43 ATTTAAAGCTTGGCCGAGCGGGCTCGCCCTCCCACTCGGCAGGCTCGGGAGGAG 102

QY 61 CCGCACCCCGCGGCCAGCCCATGACCCATGACCTCCGAGCAGGGAGTCTGTGGGGA 120

DB 103 CCGCACCCCGCGGCCAGCCCATGACCTCCGAGCAGGGAGTCTGTGGGGA 162

QY 121 TGTAGCGTGTGTGCAAGGTGTCTTGGACCTCTCCCTGCGAGTCCAGCTCTCAATCGCA 180

DB 163 TGTAGCGTGTGTGCAAGGTGTCTTGGACCTCTCCCTGCGAGTCCAGCTCTCAATCGCA 222

QY 181 CAGGGACCCAGGGCTGGCCCTCCATCCAGAAACCTATGACCTCACCGCTACTGTG 240

DB 223 CAGGGACCCAGGGCTGGCCCTCCATCCAGAAACCTATGACCTCACCGCTACTGTG 282

QY 241 AGCACCAACTCCGACGCTTGGCTGGGACCTATCTGAATACCTGGGCCCCCTTTCAAG 300

DB 283 AGCACCAACTCCGACGCTTGGCTGGGACCTATCTGAATACCTGGGCCCCCTTTCAAG 342

QY 301 AGCAGACTTCACCTCCCGGCTGGGGCGAGAGACTCTGCCAGGGCCACTGTTGACT 360

DB 343 AGCAGACTTCACCTCCCGGCTGGGGCGAGAGACTCTGCCAGGGCCACTGTTGACT 402

QY 361 TGGAGGTGTGGCGAAGCCTCAATGACAAACTGGGGCTGACCCAGAACTACGAGGCTACA 420

DB 403 TGGAGGTGTGGCGAAGCCTCAATGACAAACTGGGGCTGACCCAGAACTACGAGGCTACA 462

QY 421 GCCACCTTCTGTGTACTTGGCTGGGCTCAACCGTCAGGCTGCCACTGCTGAGCTCGGC 480

DB 463 GCCACCTTCTGTGTACTTGGCTGGGCTCAACCGTCAGGCTGCCACTGCTGAGCTCGGC 522

QY 481 GCAGCTTGGCCCACTTCTGCACACAGCTCCAGGGCTGTGGGCGAGCAATTGGGGCGTCA 540

DB 523 GCAGCTTGGCCCACTTCTGCACACAGCTCCAGGGCTGTGGGCGAGCAATTGGGGCGTCA 582

QY 541 TGGCAGCTCTGGGCTACCCACTGCCCGCAGCCGCTGCTGGGACTGAACCCACTTGACTC 600

DB 583 TGGCAGCTCTGGGCTACCCACTGCCCGCAGCCGCTGCTGGGACTGAACCCACTTGACTC 642

QY 601 CTGGCCCTGCCACAGTGTCTCTCCAGAAAGTGGACGACTTCTGGCTGCTCAAGGAGC 660

DB 643 CTGGCCCTGCCACAGTGTCTCTCCAGAAAGTGGACGACTTCTGGCTGCTCAAGGAGC 702

QY 661 TGCAGACCTGGCTGTGGCGCTCGGCCAAGGACTTCAACCGGCTCAAGAAGAGATGAGC 720

DB 703 TGCAGACCTGGCTGTGGCGCTCGGCCAAGGACTTCAACCGGCTCAAGAAGAGATGAGC 762

QY 721 CTCAGCAGCTGAGTCAACCTGCACCTGGGGCTCATGGCTTCTGACTTCTGACCTTCT 780

DB 763 CTCAGCAGCTGAGTCAACCTGCACCTGGGGCTCATGGCTTCTGACTTCTGACCTTCT 822

QY 781 CCTCTTCGCTCCCCC 795

DB 823 CCTCTTCGCTCCCCC 837

RESULT 7

AAH99772
 ID AAH99772 standard; cDNA; 768 BP.
 XX

Claim 31; Page 112-114; 123pp; English.

The present invention relates to a biologically active complex comprising a haemopoietin receptor, NFκ and cardiotrophin-like cytokine (CLC). The complex is useful in the manufacture of a medicament for the treatment and/or prophylaxis of a subject, as it is involved in facilitating proliferation, differentiation and/or survival of a cell. The complex or its components have neurotrophic activity. The present sequence is human cardiotrophin-like cytokine (CLC) cDNA

XX
Sequence 729 BP; 132 A; 261 C; 196 G; 140 T; 0 U; 0 Other;
XX

Query Match 89.1%; Score 710; DB 4; Length 729;
Best Local Similarity 100.0%; Pred. No. 6.8e-156;
Matches 710; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	86	CCCCATGACCTCCGAGCAGGGGACTCGTGGGGGATGTTAGCGTGCGTCGACCGTGCT	145
DB	7	CCCCATGACCTCCGAGCAGGGACTCGTGGGGGATGTTAGCGTGCGTCGACCGTGCT	66
QY	146	CTGGCACCTCCCTGCAGTGCAGCTCTCATTCGCAAGGGACCCAGGCCCTGGGCCCTC	205
DB	67	CTGGCACCTCCCTGCAGTGCAGCTCTCAATCGCACAGGGAGCCCAGGCCCTGGGCCCTC	126
QY	206	CATCCAGAAAACCTATGACCCTCACCGCTACCTGGAGACCACTCCGCAGCTTGCGCTGG	265
DB	127	CATCCAGAAAACCTATGACCCTCACCGCTACCTGGAGACCACTCCGCAGCTTGCGCTGG	186
QY	266	GACCTATCTGAATACCTGGGCCCCCTTTCAAAGAGCCAGACTTCAACCTTCCCGGCT	325
DB	187	GACCTATCTGAATACCTGGGCCCCCTTTCAAAGAGCCAGACTTCAACCTTCCCGGCT	246
QY	326	GGGGCAGAGACTCTGCCCGAGGCCACTGTGTGCTTGAGGTTGGCGAAGCCTCAATGA	385
DB	247	GGGGCAGAGACTCTGCCCGAGGCCACTGTGTGCTTGAGGTTGGCGAAGCCTCAATGA	306
QY	386	CAAACTGGCGCTGACCCAGAACTACGAGGCTACAGCCACTTCTGTATTCTGCGTGG	445
DB	307	CAAACTGGCGCTGACCCAGAACTACGAGGCTACAGCCACTTCTGTATTCTGCGTGG	366
QY	446	CCTCAACGTCAGGCTGCACCTGTGAGCTGGCGCGAGCGCTGCCACTTCTGCACGAG	505
DB	367	CCTCAACGTCAGGCTGCACCTGTGAGCTGGCGCGAGCGCTGCCACTTCTGCACGAG	426
QY	506	CCTCCAGGCGCTGTCTGGCGAGCATTTGGCGGCGTCATGGCAGCTCTGGGCTACCCACTGCC	565
DB	427	CCTCCAGGCGCTGTCTGGCGAGCATTTGGCGGCGTCATGGCAGCTCTGGGCTACCCACTGCC	486
QY	566	CCAGCGCTGCTGGGAGTAACCCACTTGGAATCTCTGGCCCTGGCCCCACAGTGAATTCT	625
DB	487	CCAGCGCTGCTGGGAGTAACCCACTTGGAATCTCTGGCCCTGGCCCCACAGTGAATTCT	546
QY	626	CCAGAAGATGACAGCTTCTGGCTGCTGAAGGAGCTGCAGACTGGGCTGTGGCGCTCGCG	685
DB	547	CCAGAAGATGACAGCTTCTGGCTGCTGAAGGAGCTGCAGACTGGGCTGTGGCGCTCGCG	606
QY	686	CAAGACTTCAACCGGCTCAAGAAAGAGATGCAGCTCCAGCAGCTGCAGTCAACCTGCA	745
DB	607	CAAGACTTCAACCGGCTCAAGAAAGAGATGCAGCTCCAGCAGCTGCAGTCAACCTGCA	666
QY	746	CTTGGGGCTCATGGCTTCTGACTTCTGACTTCTGACTTCTCTTGGCTCCCC	795
DB	667	CTTGGGGCTCATGGCTTCTGACTTCTGACTTCTGACTTCTCTTGGCTCCCC	716

RESULT 10
AAK51548
ID AAK51548 standard; cDNA; 1008 BP.
XX AC
XX AC AAK51548;
XX DT 06-NOV-2001 (first entry)

XX	Human polynucleotide SEQ ID NO 93.
DE	
DE	Human; cytokine; cell proliferation; cell differentiation; gene therapy;
XX	vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW	tissue growth factor; immunomodulatory; cancer; leukaemia;
KW	nervous system disorder; arthritis; inflammation; ss.
XX	
XX	Homo sapiens.
OS	
XX	WO200157190-A2.
PN	
XX	09-AUG-2001.
PD	
XX	
PF	05-FEB-2001; 2001WO-US004098.
PP	
XX	03-FEB-2000; 2000US-00496914.
PR	27-APR-2000; 2000US-00560875.
PR	20-JUN-2000; 2000US-00598075.
PR	19-JUL-2000; 2000US-00820325.
PR	01-SEP-2000; 2000US-00854936.
PR	15-SEP-2000; 2000US-00863561.
PR	20-OCT-2000; 2000US-00693325.
PR	30-NOV-2000; 2000US-00728422.
XX	
PA	(HYSE-) HYSEQ INC.
XX	
PI	Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
PI	Ma Y, Zhao Qa, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI	Xue AJ, Yang Y, Wejhrman T, Goodrich R;
DR	WPI; 2001-476283/51.
DR	P-PSDB; AAM78415.
XX	
XX	Nucleic acids encoding polypeptides with cytokine-like activities, useful
PT	in diagnosis and gene therapy.
PT	
XX	Claim 1; Page 711-712; 6221pp; English.
XX	
CC	The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC	encoded polypeptides (AAM78323-AAM90302) that exhibit activity elating to
CC	cytokine, cell proliferation or cell differentiation or which may induce
CC	production of other cytokines in other cell populations. The
CC	polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC	peptide therapy. The polypeptides have various cytokine-like activities,
CC	e.g. stem cell growth factor activity, haematopoiesis regulating
CC	activity, tissue growth factor activity, immunomodulatory activity and
CC	activin/inhibin activity and may be useful in the diagnosis and/or
CC	treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC	inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
CC	(AAK52582) and 3566 (AAM80020) are omitted as the relevant pages from the
CC	sequence listing were missing at the time of publication
XX	
SQ	Sequence 1008 BP; 183 A; 374 C; 247 G; 204 T; 0 U; 0 Other;
	Query Match 87.2%; Score 694.8; DB 4; Length 1008;
	Best Local Similarity 97.0%; Pred. No. 2.6e-152;
	Matches 708; Conservative 0; Mismatches 22; Indels 0; Gaps 0
QY	66 CCGCGCCGCGCCAGCCCGCCAGCCCATGCAGCTCGAGCAGGGGACCTCGTGGGGGATGTTA 125
Db	267 CCGCGCGCGCGCTATGCTTCGTTCATCTGCCACAGGGGACCTCGTGGGGGATGTTA 326
QY	126 GCGTCCCTGTGCACGCTGCTCTGGACCTCCCTGCACTGCCAGTCCAGCTCTCAATCCACAGG 185
Db	327 GCGTCCCTGTGCACGCTGCTCTGGACCTCCCTGCACTGCCAGTCCAGCTCTCAATCCACAGG 386
QY	186 GACCCAGGCGCTGCGCCCTGCATCCAGAAACCTATGACCTCACCGCTACTCTGGAGCAC 245
Db	387 GACCCAGGCGCTGCGCCCTGCATCCAGAAACCTATGACCCACCGCTACTCTGGAGCAC 446
QY	246 CAACCTCCGACGCTTGGTGGGACCTATCTGAATCTACTGGGCGCCCTTTCAACAGGCCA 305

447	Db	CAACTCCGCAAGCTTTGGCTGGGAACCTATCTGAACTA	CTGGGCCCCCTTTCAACAGCA	506
306	Qy	GACTTTAAACCCCTCCCGCTGGGGGCAAGACTCTGCCAGGSCCACTGTTGACTTGGAG		365
507	Db	GACTTTAAACCCCTCCCGCTGGGGGCAAGACTCTGCCAGGSCCACTGTTGACTTGGAG		566
366	Qy	GTGTGGCAAGCCTCAATGACAAACTGGGCTGACCAGCAACTACGAGCCTACAGCCAC		425
567	Db	GTGTGGCAAGCCTCAATGACAAACTGGGCTGACCAGCAACTACGAGCCTACAGCCAC		626
426	Qy	CTTCTGTGTTACTTGGCTGGGCTCAACCGTCAGGCTGCCACTGCTGAGTGTGGCCGCGAC		485
627	Db	CTTCTGTGTTACTTGGCTGGGCTCAACCGTCAGGCTGCCACTGCTGAGTGTGGCCGCGAC		686
486	Qy	CTGGGCCACTTCTGCACCAAGCCTCAGGGCTCTGGGAGCACTTCGGGGCTCATGSCA		545
687	Db	CTGGGGCCACTTCTGCACCAAGCCTCAGGGCTCTGGGAGCACTTCGGGGCTCATGSCA		746
546	Qy	GCTCTGGGCTACCACTGCCCCCAGCCGCTGCCTGGGACTGAACCCACTTGGACTCTCTGGC		605
747	Db	GCTCTGGGCTACCACTGCCCCCAGCCGCTGCCTGGGACTGAACCCACTTGGACTCTCTGGC		806
606	Qy	CTGGGCCACAGTGACTTCTCCAGAAAGATGAGACACTTCTGGCTGTGAAGAGAGTGCAG		665
807	Db	CTGGGCCACAGTGACTTCTCCAGAAAGATGAGACACTTCTGGCTGTGAAGAGAGTGCAG		866
666	Qy	ACCTGGCTGTGGCGCTCGGCCAAGGACTTCAACCGGCTCAAGAAAGATGACAGCTCCA		725
867	Db	ACCTGGCTGTGGCGCTCGGCCAAGGACTTCAACCGGCTCAAGAAAGATGACAGCTCCA		926
726	Qy	GCAGCTGCAGTCAACCTGCACTCGGGGCTCATGGCTTCTGACTTCTGACCTTCTCCTCT		785
927	Db	GCAGCTGCAGTCAACCTGCACTCGGGGCTCATGGCTTCTGACTTCTGACCTTCTCCTCT		986
786	Qy	TGCTCCCCC		795
987	Db	TGCTCCCCC		996

RESULT 11

RESUL II
AAV22654

AAV22654
ID AAV22654 standard; cDNA: 819 BP.

XX
AC AAV22654:XX
DT 13-III.-1998 (first entry)

BT 13-JUL-1998 (first entry)
yy

XX
DE
CDNA encoding murine neurotrophic factor NNT-1.

Mouse; neurotrophic factor; NNT-1; growth; motor; sympathetic; neuron;
treatment; neurological disease; degeneration; Parkinson's disease;
amyotrophic lateral sclerosis. AIS; Alzheimer's disease; stroke; ss.

2000 2001 2002 2003 2004 2005 2006 2007 2008 2009 2010 2011 2012 2013 2014 2015 2016 2017 2018 2019 2020 2021 2022 2023 2024 2025 2026 2027 2028 2029 2030 2031 2032 2033 2034 2035 2036 2037 2038 2039 2040 2041 2042 2043 2044 2045 2046 2047 2048 2049 2050 2051 2052 2053 2054 2055 2056 2057 2058 2059 2060 2061 2062 2063 2064 2065 2066 2067 2068 2069 2070 2071 2072 2073 2074 2075 2076 2077 2078 2079 2080 2081 2082 2083 2084 2085 2086 2087 2088 2089 2090 2091 2092 2093 2094 2095 2096 2097 2098 2099 2100 2101 2102 2103 2104 2105 2106 2107 2108 2109 2110 2111 2112 2113 2114 2115 2116 2117 2118 2119 2120 2121 2122 2123 2124 2125 2126 2127 2128 2129 2130 2131 2132 2133 2134 2135 2136 2137 2138 2139 2140 2141 2142 2143 2144 2145 2146 2147 2148 2149 2150 2151 2152 2153 2154 2155 2156 2157 2158 2159 2160 2161 2162 2163 2164 2165 2166 2167 2168 2169 2170 2171 2172 2173 2174 2175 2176 2177 2178 2179 2180 2181 2182 2183 2184 2185 2186 2187 2188 2189 2190 2191 2192 2193 2194 2195 2196 2197 2198 2199 2200 2201 2202 2203 2204 2205 2206 2207 2208 2209 2210 2211 2212 2213 2214 2215 2216 2217 2218 2219 2220 2221 2222 2223 2224 2225 2226 2227 2228 2229 2230 2231 2232 2233 2234 2235 2236 2237 2238 2239 2240 2241 2242 2243 2244 2245 2246 2247 2248 2249 2250 2251 2252 2253 2254 2255 2256 2257 2258 2259 2260 2261 2262 2263 2264 2265 2266 2267 2268 2269 2270 2271 2272 2273 2274 2275 2276 2277 2278 2279 2280 2281 2282 2283 2284 2285 2286 2287 2288 2289 2290 2291 2292 2293 2294 2295 2296 2297 2298 2299 2300 2301 2302 2303 2304 2305 2306 2307 2308 2309 2310 2311 2312 2313 2314 2315 2316 2317 2318 2319 2320 2321 2322 2323 2324 2325 2326 2327 2328 2329 2330 2331 2332 2333 2334 2335 2336 2337 2338 2339 2340 2341 2342 2343 2344 2345 2346 2347 2348 2349 2350 2351 2352 2353 2354 2355 2356 2357 2358 2359 2360 2361 2362 2363 2364 2365 2366 2367 2368 2369 2370 2371 2372 2373 2374 2375 2376 2377 2378 2379 2380 2381 2382 2383 2384 2385 2386 2387 2388 2389 2390 2391 2392 2393 2394 2395 2396 2397 2398 2399 2400 2401 2402 2403 2404 2405 2406 2407 2408 2409 2410 2411 2412 2413 2414 2415 2416 2417 2418 2419 2420 2421 2422 2423 2424 2425 2426 2427 2428 2429 2430 2431 2432 2433 2434 2435 2436 2437 2438 2439 2440 2441 2442 2443 2444 2445 2446 2447 2448 2449 2450 2451 2452 2453 2454 2455 2456 2457 2458 2459 2460 2461 2462 2463 2464 2465 2466 2467 2468 2469 2470 2471 2472 2473 2474 2475 2476 2477 2478 2479 2480 2481 2482 2483 2484 2485 2486 2487 2488 2489 2490 2491 2492 2493 2494 2495 2496 2497 2498 2499 2500 2501 2502 2503 2504 2505 2506 2507 2508 2509 2510 2511 2512 2513 2514 2515 2516 2517 2518 2519 2520 2521 2522 2523 2524 2525 2526 2527 2528 2529 2530 2531 2532 2533 2534 2535 2536 2537 2538 2539 2540 2541 2542 2543 2544 2545 2546 2547 2548 2549 2550 2551 2552 2553 2554 2555 2556 2557 2558 2559 2560 2561 2562 2563 2564 2565 2566 2567 2568 2569 2570 2571 2572 2573 2574 2575 2576 2577 2578 2579 2580 2581 2582 2583 2584 2585 2586 2587 2588 2589 2590 2591 2592 2593 2594 2595 2596 2597 2598 2599 2600 2601 2602 2603 2604 2605 2606 2607 2608 2609 2610 2611 2612 2613 2614 2615 2616 2617 2618 2619 2620 2621 2622 2623 2624 2625 2626 2627 2628 2629 2630 2631 2632 2633 2634 2635 2636 2637 2638 2639 2640 2641 2642 2643 2644 2645 2646 2647 2648 2649 2650 2651 2652 2653 2654 2655 2656 2657 2658 2659 2660 2661 2662 2663 2664 2665 2666 2667 2668 2669 2670 2671 2672 2673 2674 2675 2676 2677 2678 2679 2680 2681 2682 2683 2684 2685 2686 2687 2688 2689 2690 2691 2692 2693 2694 2695 2696 2697 2698 2699 2700 2701 2702 2703 2704 2705 2706 2707 2708 2709 2710 2711 2712 2713 2714 2715 2716 2717 2718 2719 2720 2721 2722 2723 2724 2725 2726 2727 2728 2729 2730 2731 2732 2733 2734 2735 2736 2737 2738 2739 2740 2741 2742 2743 2744 2745 2746 2747 2748 2749 2750 2751 2752 2753 2754 2755 2756 2757 2758 2759 2760 2761 2762 2763 2764 2765 2766 2767 2768 2769 2770 2771 2772 2773 2774 2775 2776 2777 2778 2779 2780 2781 2782 2783 2784 2785 2786 2787 2788 2789 2790 2791 2792 2793 2794 2795 2796 2797 2798 2799 2800 2801 2802 2803 2804 2805 2806 2807 2808 2809 2810 2811 2812 2813 2814 2815 2816 2817 2818

XX	key	Location/Qualifiers
FH	CDS	95..771
FT		/*tag= a
FT	sig_peptide	95..175
FT		/*tag= b
FT	mat_peptide	176..769
FT		/*tag= c

XX PN US5741772-A.

XX
XX
US314145A.

21-APR-1998.

XX
ED-ATK-1000;

PF 03-FEB-1997;

XX

PR 03-FEB-1997;

XX

PA (AMGE-) AMGE-

XX

PI	Chang M;	
XX		
DR	WPI; 1998-260526/23.	
DR	P-PSDB; AAM56142.	
XX		
PT	Neurotrophic factor NNT-1 polypeptide and related nucleic acids - useful	
PT	for stimulating growth of motor and sympathetic neurons.	
XX		
XX	Disclosure; Fig 4; 4ipp; English.	
XX		
CC	The present sequence encodes a murine neurotrophic factor, designated NNT	
CC	-1, which is capable of stimulating growth of motor or sympathetic	
CC	neurons. The NNT-1 protein is useful in the treatment of neurological	
CC	diseases characterised by the degeneration and death of particular	
CC	classes of neurons. These diseases specifically include Parkinson's	
CC	disease, amyotrophic lateral sclerosis (ALS), Alzheimer's disease, stroke	
CC	and various degenerative disorders affecting vision	
XX		
XX	Sequence 819 BP; 156 A; 288 C; 218 G; 157 T; 0 U; 0 Other;	
XX		
XX		

PA 111

```

Db      725 CCTCCAGAGCTTCAGTACCCCTGCACTTGGAGGACATGTTCTGACCTTGACCT 783
RESULT 12
AAV47512
ID      AAV47512 standard; cDNA; 819 BP.
AC      AAV47512;
XX
XX
XX      09-NOV-1998 (first entry)
XX      Mouse neurotrophic factor NNT-1 cDNA.
XX
XX      NNT-1; neurotrophic factor; mouse; antiinflammatory; adjuvant;
XX      Alzheimer's disease; Parkinson's disease; Huntington's disease;
XX      amyotrophic lateral sclerosis; Charcot-Marie-Tooth syndrome;
XX      peripheral neuropathy; dystrophy; neural retina degeneration;
XX      common variable immunodeficiency; CVID; selective IGA deficiency;
XX      hypogammaglobulinaemia; X-linked agammaglobulinaemia; antiseptic;
XX      therapy; ss.
XX
XX      Mus sp.
XX
XX      Key      Location/Qualifiers
XX      CDS      95..772
XX              /*tag= a
XX      sig_peptide 95..175
XX              /*tag= b
XX      mat_peptide 176..769
XX              /*tag= c
XX
XX      WO9833922-A1.
XX
XX      06-AUG-1998.
XX
XX      02-FEB-1998; 98WO-US002363.
XX
XX      03-FEB-1997; 97US-00792019.
XX      30-JAN-1998; 98US-00016534.
XX
XX      (ANGE-) AMGEN INC.
XX
XX      Chang M, Elliot GS, Senaldi G, Sarmiento U;
XX
XX      WPI; 1998-437475/37.
XX      P-PSDB; AAV29716.
XX
XX      Newly isolated nucleic acid encoding human or murine neurotrophic factor
XX      NNT-1 - useful for treatment of neurological and immunological diseases
XX      or inflammation, also as vaccine adjuvant.
XX
XX      Disclosure; Fig 4; 120pp; English.
XX
XX      This newly isolated mouse cDNA sequence codes for a novel neurotrophic
XX      factor, designated NNT-1 (see AAV29716), that is a growth factor for
XX      neurons and for B or T cells. Vectors and host cells are provided for use
XX      in the production of murine and human NNT-1 polypeptides. These are used
XX      to treat: (i) neurological or immunological diseases, specifically
XX      Alzheimer's, Parkinson's or Huntington's diseases, amyotrophic lateral
XX      sclerosis, Charcot-Marie-Tooth syndrome, peripheral neuropathy, dystrophy
XX      and degeneration of the neural retina, or conditions characterised by T
XX      or B cell defects, e.g. common variable immunodeficiency (CVID),
XX      selective IGA deficiency, hypogammaglobulinaemia and X-linked
XX      agammaglobulinaemia (claimed), but many others disclosed; and (ii)
XX      inflammation. NNT-1 is also able to boost immunoreactivity and antibody
XX      production following vaccination, and, since it inhibits tumour necrosis
XX      factor production, it may also be useful for treating sepsis. NNT-1
XX      nucleic acid fragments are also used as hybridisation probes in
XX      diagnostic assays. In addition, cells that have been engineered to
XX      express NNT-1 can be implanted, or nucleic acids are delivered in gene
XX      therapy vectors

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SQ      Sequence 819 BP; 156 A; 288 C; 218 G; 157 T; 0 U; 0 Other;
Query Match      84.0%; Score 669.4; DB 2; Length 819;
Best Local Similarity 92.0%; Pred. No. 28-146;
Matches 717; Conservative 0; Mismatches 61; Indels 1; Gaps 1;
QY      1 ATTAAGCTTCGCGGAGCGCGGCTCCCTCCCACTCCGCGAGGCTCCGCGAGGAG 60
Db      5 ATTAAGCTTCGCGGAGCGCGGCTCCCTCCCACTCCGCGAGGCTCCGCGAGGAG 64
QY      61 CCGCACCGCGCGCGCCAG - CCGCAGCCCATGGACCTCCGAGCAGGGAGCTCGTGGGG 119
Db      65 CCGCGCGCGCGCGCGCCAGCCCGCCAGCTCCGAGCAGGGAGCTCGTGGGG 124
QY      120 ATGTTAGCGTGTGCAACGGTGTCTGGACCTCCCTGAGTGCAGTCTCAATCGC 179
Db      125 ATGTTAGCTTGCTATGACCGTGTGTGGACCTCCCTGAGTGCAGTCTTAAATCGC 184
QY      180 ACAGGGAGCCCAAGGCGCTGGCCCTCCCATCCAGAAAACCTATGACCTCACCGCTACCTG 239
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QY      240 GAGCACCAACTCCGAGCTTGGCTGGGACCTATCTGAACCTAGCTGGGCGCCCTTTCAAC 299
Db      245 GAGCATCAACTCCGAGCTTAGCTGGGACCTACCTGAACTACCTGGGGCGCCCTTTCAAC 304
QY      300 GAGCCAGACTTCAACCCCTCCCGCGCTGGGGGAGAGACTCTGCCAGAGCCACTGTGTAC 359
Db      305 GAGCTTGACTTCAATCTCTCTGCACTGGGGGAGAGAACTCTGCCAGAGGCGACGTCAAC 364
QY      360 TTGGAGGTGTGGAGAGCTCAATCAAACTGCGGCTGACCCAGAACTACAGAGGCTTAC 419
Db      365 TTGGAGGTGTGGAGAGGCTCAATGACAGGCTGCGGCTGACCCAGAACTATGAGGCGTAC 424
QY      420 AGCCACCTTCTGTGTACTTGGTGGCGCTCAACCTCAGGCTGCCACTGTGAGTGGCG 479
Db      425 AGTCACCTCTCTGTGTACTTGGTGGCGCTCAACCTCAGGCTGCCACTGTGAGTGGCG 484
QY      480 CGCAGCTGGCCCACTTCTGACACAGCCTTCCAGGCGCTGCTGGGAGCAGATTCCGGGCGTC 539
Db      485 CGTAGCTGGCCCACTTCTGTATACAGCTTCCAGGCGCTGCTGGGAGCAGATTCCAGGTGC 544
QY      540 ATGGCAGCTTGGGCTACCCACTGCCCGCGCTGCCCTGGGAGCTGAACCCACTTGGACT 599
Db      545 ATGGCAGCTTGGGCTACCCACTGCCCGCGCTGCCCTGGGAGCTGAACCCACTTGGGCG 604
QY      600 CTGGGCGCTGCCAGAGTACTTCTCCAGAAAGATGGACACTTCTGGCTGTCTGAAGGAG 659
Db      605 CTGGGCGCTGCCAGAGTACTTCTCCAGAAAGATGGAGTACTTCTGGCTGTCTGAAGGAG 664
QY      660 CTGCAGACTGCTGTGGCGCTCGGCGCAAGGACTTCAACCGGCTCAAGAAAGATGCGAG 719
Db      665 CTGCAGACTGCTGTGGCGTTTCCAGCAAGGACTTCAACCGGCTTAAAGAAAGATGCGAG 724
QY      720 CTTCCAGAGCTGCACTGACCTCCCTGAGCGGCTCATGGCTTCTGACTTCTGACCTT 778
Db      725 CTTCCAGAGCTTCACTGACCTCCCTGAGCGGCGCATGGTTTCTGACCTTCTGACCTT 783
RESULT 13
AAV39483
ID      AAV39483 standard; cDNA; 819 BP.
XX
XX      AAV39483;
XX
XX      24-AUG-2000 (first entry)
XX
XX      Murine NNT-1 cDNA.
XX
XX      NNT-1; neurotrophic factor; nootropic; neuroprotective; treatment;
XX      anticonvulsant; antiparkinsonian; antidiabetic; ophthalmological;
XX      nervous system degeneration; Alzheimer's disease; Parkinson's disease;
XX      amyotrophic lateral sclerosis; Charcot-Marie-Tooth syndrome; murine;

```


KW Huntington's disease; peripheral neuropathy; neural retina degeneration;
 KW retinopathy; immune disorder; hematopoietic disorder; ss.
 XX
 OS Mus sp.
 FH .Key Location/Qualifiers
 FT CDS 95..772
 FT /*tag= a
 FT /product= "NNT-1"
 XX
 PN US6054294-A.
 XX
 XX
 PD 25-APR-2000.
 XX
 XX 12-DEC-1997; 97US-00988819.
 XX
 PR 03-FEB-1997; 97US-00792019.
 XX
 XX (AMGE-) AMGEN INC.
 XX
 XX Chang M;
 XX
 XX WPI: 2000-338492/29.
 DR P-PSDB; AA187814.
 DR
 XX
 PT New nucleic acids encoding neurotrophic factors useful for stimulating
 PT growth of motor or sympathetic neurons for treating neuron cell damage.
 XX
 PS Claim 2a; Fig 4; 42pp; English.
 XX
 CC This invention describes a novel nucleic acid molecule (I) encoding a
 CC novel neurotrophic factor (NNT-1) (II) which has nootropic,
 CC neuroprotective, anticonvulsant, antiparkinsonian, antidiabetic and
 CC ophthalmological activity. (II) is useful for producing NNT-1 polypeptides
 CC which are useful for treating patients in whom various cells of the
 CC central, autonomic, or peripheral nervous system have degenerated and/or
 CC have been damaged by congenital disease, trauma, mechanical damage,
 CC surgery, stroke, ischemia, infection, metabolic disease, nutritional
 CC deficiency, malignancy and/or toxic agents. NNT-1 proteins are used to
 CC treat diseases like Alzheimer's, Parkinson's, amyotrophic lateral
 CC sclerosis, Charcot-Marie-Tooth syndrome, Huntington's disease, peripheral
 CC neuropathy induced by diabetes or other metabolic disorders, and/or
 CC dystrophies or degeneration of the neural retina such as retinitis
 CC pigmentosa, drug-induced retinopathies, stationary forms of night
 CC blindness, progressive cone-rod degeneration, immune disorders and
 CC hematopoietic disorders. (II) is effective in treating neurological
 CC conditions and promotes neuron regeneration. Neural functions are
 CC effectively restored in patients suffering from various neurological
 CC disorders. This sequence encodes the murine NNT-1 protein described in
 CC the method of the invention
 XX
 SQ Sequence 819 BP; 156 A; 288 C; 218 G; 157 T; 0 U; 0 Other;
 Query Match 84.0%; Score 669.4; DB 3; Length 819;
 Best Local Similarity 92.0%; Pred. No. 2e-146;
 Matches 71.7; Conservative 0; Mismatches 61; Indels 1; Gaps 1;
 1 ATTAAAGCTTCGGGAGCGGGCTCGCCCTCCGACCTCCGACGCTCCGGGAGGAG 60
 5 ATTAAAGCTTCGGGAGCGGGCTCGCCCTCCGACCTCCGACGCTTCGGGAGGAG 64
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 65 CGGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 124
 120 ATGTTAGCTGCTGTGACGGTGTCTGGACCTCCGACCTCCGACGCTTCATCGC 179
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QY 240 GAGCACAACCTCCGAGCTTGGCTGGGACCTATCTCTGAACCTAGCTGGGCCCCCTTTCAAC 299
 DB 245 GAGCATCAACTCCGAGCTTAGCTGGGACCTACCTGACTTGGGGCCCCCTTTCAAC 304
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 DB 305 GAGCCTGACTTCAATCTCTCTGACTTGGGGGAGAAACTCTGCCAGGGCCAGCGTCAAC 364
 QY 360 TTGGAGGTGGGGAAGCCCTCAATGACAAACTGCGGCTGACCCAGAACTACGAGGCTAC 419
 DB 365 TTGGAGGTGGGGAAGCCCTCAATGACAGGCTGCGGCTGACCCAGAACTATGAGGGGTAC 424
 QY 420 AGCCACCTTCTGTGTTACTTGGCTGAGCTCAACCCGTCAGGCTGCCACTGCTGAGCTGGCG 479
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 QY 540 ATGCGAGCTCTGGGCTACCCACTGCCCCAGCGCTGCTGGGAGTGAACCCACTTGGACT 599
 DB 545 ATGCGAGGCTTGGCTTACCCACTGCCCCAGCTTCCGAGGAGCTGAGCAGCTGGGCGC 604
 QY 600 CTTGGCCCTGCCCACAGTGAATCTCTCCAGAGATGAGAGACTTCTGGCTGCTGAGGAG 659
 DB 605 CTTGGCCCTGCCCACAGTGAATCTCTCCAGAGATGAGAGACTTCTGGCTGCTGAGGAG 664
 QY 660 CTGCGAGCTTGGCTGTTGGGCTTGGGCAAGGAGCTTCAACCGGCTCAAGAAGAGATGCAG 719
 DB 665 CTGCGAGCTTGGCTGTTGGGCTTGGGCAAGGAGCTTCAACCGGCTTAAAGAAGAGATGCAG 724
 QY 720 CTTCCAGAGCTGCACTGACCTGACCTGCGAGCTGCTGGGGCTGCTGAGCTTCTGACCTT 778
 DB 725 CTTCCAGAGCTTCACTGACCTGCACTTGGAGGACATGTTTCTGACCTCTGACCTT 783
 RESULT 14
 ABK11649
 ID ABK11649 standard; cDNA; 819 BP.
 XX
 AC ABK11649;
 XX
 DT 05-JUN-2002 (first entry)
 XX
 DE Mouse cDNA encoding novel neurotrophic factor NNT1.
 XX
 KW Mouse; ss; gene; NNT1; neurotrophic factor; IgE-related disease;
 KW Type I allergic disease; allergic rhinitis; eczema; dermatitis;
 KW pollinosis; asthma; immune disease; cancer; arteriosclerosis;
 KW vascular restenosis; rheumatoid arthritis; psoriatic arthritis;
 KW inflammatory arthritis; osteoarthritis; inflammatory joint disease;
 KW autoimmune disease; multiple sclerosis; lupus; diabetes; endometriosis;
 KW inflammatory bowel disease; transplant rejection; reproductive disorder;
 KW graft versus host disease; infertility; miscarriage; preterm labour.
 XX
 OS Mus sp.
 XX
 FH .Key Location/Qualifiers
 FT CDS 95..772
 FT /*tag= a
 FT /product= "NNT1"
 XX
 PN WO200215977-A2.
 XX
 PD 28-FEB-2002.
 XX
 XX 17-AUG-2001; 2001WO-US025906.
 XX
 XX 18-AUG-2000; 2000US-0226436P.
 PR 16-AUG-2001; 2001US-00931704.
 XX
 XX (AMGE-) AMGEN INC.
 PA

XX PI Senaldi G;
 XX DR WPI; 2002-280867/32.
 XX DR P-PSDB; AAU78177.
 XX PT Treating Immunoglobulin E-related disease, modulating IgE levels in a
 PT patient, preventing IgE-related disease and treating allergic diseases,
 PT involves administering NN1-1 inhibitor to a patient.
 XX PS Claim 2; Fig 4; 63pp; English.
 XX CC The invention relates to treating Immunoglobulin E (IgE)-related disease,
 CC modulating IgE levels in a patient, preventing an IgE-related disease,
 CC and treating allergic diseases, comprising administering a
 CC therapeutically effective amount of novel neurotrophic factor (NN1)-1
 CC inhibitor to a patient. Also included are a method of diagnosing an IgE-
 CC related disease or susceptibility to an IgE-related disease, by
 CC determining the presence or amount of expression of an NN1 polypeptide
 CC encoded by a NN1 nucleotide sequence, its fragment or naturally
 CC occurring variant, and diagnosing an IgE-related disease or
 CC susceptibility of an IgE-related disease based on the presence or amount
 CC of expression of the polypeptide and a pharmaceutical composition for use
 CC in treating IgE-related disease, comprising the NN1 inhibitor. The NN1
 CC inhibitor is useful for preventing and treating IgE-related disease,
 CC modulating IgE levels, and treating allergic diseases e.g. Type I
 CC allergic disease, allergic rhinitis, eczema, dermatitis, pollinosis,
 CC asthma, immune diseases and disorders, diseases involving abnormal cell
 CC proliferation including cancer, arteriosclerosis and vascular stenosis,
 CC diseases and conditions relating to dysfunction of immune system
 CC including rheumatoid arthritis, psoriatic arthritis, inflammatory
 CC arthritis, osteoarthritis, inflammatory joint disease, autoimmune
 CC disease, multiple sclerosis, lupus, diabetes, inflammatory bowel disease,
 CC transplant rejection, and graft versus host disease, and reproductive
 CC diseases and disorders including infertility, miscarriage, preterm labour
 CC and delivery, and endometriosis. The present sequence encodes mouse NN1
 XX
 SQ Sequence 819 BP; 156 A; 288 C; 218 G; 157 T; 0 U; 0 Other;
 Query Match 84.0%; Score 669.4; DB 6; Length 819;
 Best Local Similarity 92.0%; Pred. No. 2e-146;
 Matches 717; Conservative 0; Mismatches 61; Indels 1; Gaps 1;
 QY 1 ATTTAAAGCTTCGCGGAGCGCGCTCGCTCCACTCCGACGCTCCGGAGAGGAG 60
 DB 5 ATTTAAAGCTTCGCGGAGCGCGCTCGCTCCACTCCGACGCTCCGGAGAGGAG 64
 QY 61 CCGCACCCCGCGGCCAG-CCCGACGCCATGACCTCCGAGCAGGGGACTCGTGGGG 119
 DB 65 CCGCGCCCGCGCGCCCGGCCCGCCAGCCCATGACCTCCGACGAGGGGACTCGTGGGG 124
 QY 120 ATGTTAGCGTCTGTCGACGGTGCTCTGGACCTCCCTCGAGTGCAGCTCTCAATCGC 179
 DB 125 ATGTTAGCTTGCTTATGACGGTCTCTGGACCTCCCTCGAGTGCAGCTCTTAATCGC 184
 QY 180 ACAGGGGACCCAGGCGCTGCCCTCCATCCAGAAACCTATGACCTCACCGCTACCTG 239
 DB 185 ACAGGAGATCAGGCGCTTGCCCTCCATCCAGAAACCTATGACCTCACCGCTACCTG 244
 QY 240 GAGCACCAACTCCGACGCTTGCTGGGACCTATCTGAACCTACCTGGGCCCCCTTTCAAC 299
 DB 245 GAGCATCAACTCCGACGCTTAGCTGGGACCTATCTGAACCTACCTGGGCCCCCTTTCAAC 304
 QY 300 GAGCAGACTTCACCTCCCGCTCGGGGACAGACTCTGCCAGGGCACTGTGTGAC 359
 DB 305 GAGCCTGACTTCAATCTCTCGACTGGGGGAGAACTCTGCCAGGGGCACTGTGTGAC 364
 QY 360 TTGGAGGTGTGGCGAAGCCTCAATGACAAACTCGGGCTGACCCAGAACTACGAGGCGCTAC 419
 DB 365 TTGGAAGTGTGGCGAAGCCTCAATGACAGGCTGCGGCTGACCCAGAACTATGAGGGGTAC 424
 QY 420 AGCCACCTTCTGTGTTACTTGGTGGCTCAACCGTCAAGCTGCTGCTGAGCTGCGC 479

DB 425 AGTCACCTCCTGTGTTACTTGTGGTCCCTCAACCGTCAAGCTGCCACAGCTGAATCCGA 484
 QY 480 CCGAGCCTGGCCCACTTTGACCAACAGCCCTCCAGGGGCTGCTGGGAGCAGATTGCGGCGCTC 539
 DB 485 CGTAGCCTGGCCCACTTTGTTACCAAGCCTCCAGGGGCTGCTGGGAGCAGATTGCGAGTGTG 544
 QY 540 ATGGCAGCTCTGGGCTACCCAGTCCCGCAGCGCTGCGCTGGGAGTGAACCCCACTTGGACT 599
 DB 545 ATGGGACGCTTGGCTTACCCAGTCCCGCAGCCTGCGCCAGGACTGAGCAGCCCTGGGCC 604
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 DB 605 CTTGGCCCTGCCCAAGTCACTTCTCCAGAAAGTGGAGCACTTCTGGCTGTGTAAGGAG 664
 QY 660 CTGCAGACTGCTGTGGGCTCGGCCAAGGACTTCAACCGGCTCAAGAGAGATGAG 719
 DB 665 CTGCAGACTGCTGTGGGCTCGGCCAAGGACTTCAACCGGCTTAAAGAGAGATGAG 724
 QY 720 CTTCCAGCAGCTGCACTCACCTCGACCTGGGGGCTCATGGCTTCTGACTTCTGACCTT 778
 DB 725 CTTCCAGCAGCTTCACTCACCTCGACCTGGAGGACATGGTTTCTGACTTCTGACCTT 783
 RESULT 15
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 ID ABA09140 standard; cDNA; 968 BP.
 XX ABA09140;
 AC ABA09140;
 XX
 DT 11-JAN-2002 (first entry)
 XX Human cardiotrophin-like cytokine homologue cDNA, SEQ ID NO:916.
 DE
 XX Human; cytokine; cell proliferation; tissue growth; immunomodulator; growth factor;
 KW haematopoiesis regulation; tissue growth; immunomodulator; activin;
 KW inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
 KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
 KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
 KW chronic inflammatory condition; proliferative retinopathy;
 KW atherosclerosis; coronary heart disease; arterial ischaemia;
 KW bone disorder; osteoporosis; vascular growth disorder;
 KW tissue regeneration; wound healing; infection; immune disorder;
 KW cell culture; drug screening; gene therapy; antiinflammatory;
 KW antasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
 KW cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
 KW antifungal; vulnery; antiulcer; ss.
 XX
 OS Homo sapiens.
 XX
 FN WO200157198-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 05-FEB-2001; 2001WO-US003800.
 XX
 PR 03-FEB-2000; 2000US-00496914.
 PR 27-APR-2000; 2000US-00560875.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Drmanac RT;
 XX
 XX WPI; 2001-457740/49.
 DR F-PSDB; ABB11896.
 XX
 PT Human proteins and DNA encoding sequences useful for preventing, treating
 PT or ameliorating a medical condition in a mammalian subject e.g. arthritis
 and cancer.
 XX
 PS Claim 1; Page 793-794; 1963pp; English.
 XX
 CC Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
 CC sequences ABA08235-ABA09574 represent nucleic acids encoding them. The

CC invention also relates to vectors and recombinant host cells comprising a
CC nucleotide of the invention, methods of producing the novel polypeptides,
CC antibodies against the polypeptides, methods of detecting the nucleotides
CC or polypeptides in a sample, and methods of identifying compounds which
CC bind to polypeptides of the invention. Although novel, many of the
CC polypeptides of the invention have homology to known proteins, thereby
CC giving an insight into their probable biological activities, and hence
CC potential therapeutic applications. The polypeptides of the invention may
CC have various activities, including cytokine, cell proliferation or cell
CC differentiation activities; stem cell growth factor activity;
CC haematopoiesis regulatory activity; tissue growth activity;
CC immunomodulatory activity; activin- or inhibin-related activities;
CC chemotactic or chemokinetic activities; haemostatic, thrombotic or
CC thrombolytic activities; receptor or ligand activities; or may be
CC involved in oncogenesis, cancer cell proliferation or metastasis.
CC Depending on their biological activities, polypeptides and nucleotides of
CC the invention are useful for preventing, treating or ameliorating medical
CC conditions, e.g., by protein or gene therapy. Such conditions include
CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell
CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
CC proliferative retinopathy, atherosclerosis, coronary heart disease,
CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
CC repair (or nucleic acids encoding them) may be used to promote wound
CC healing (e.g., of burns, incisions and ulcers), while those with
CC immunomodulatory activities may be used in the treatment of viral,
CC bacterial and fungal infections in addition to immune disorders.
CC Polypeptides with growth factor activity may be used in cell cultures to
CC promote cell growth. For example, such polypeptides may be used to
CC manipulate stem cells in culture to give rise to neuroepithelial cells
CC that can be used to augment or replace cells damaged by illness,
CC autoimmune disease or accidental damage. The polypeptides and nucleotides
CC may also be used in the diagnosis of the above conditions, and in drug
CC screening techniques. The present sequence represents a cDNA encoding a
CC novel human polypeptide of the invention
XX
SQ Sequence 968 BP; 179 A; 353 C; 244 G; 192 T; 0 U; 0 Other;

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Best Local Similarity		97.0%;	Pred. No. 3.6e-146;		
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QY	66	CCCGCGCGCGCCAGCCGCCACCCACCTGAGCTCCGAGAGGCGACTCGTGGGGGATGTTA	125		
DB	267	CCCGGCGCGCGCTGATGCTTCTGCTCCATCTCTGCCACAGGGGACTCGTGGGGGATGTTA	326		
QY	126	GGTGCTGTGACCGGTGTCTGTGGACCTCCCTGTGAGTGCCAGCTCTCAATGCGACAGGG	185		
DB	327	GGTGCTGTGACCGGTGTCTGTGGACCTCCCTGCGAGTGCCAGCTCTCAATGCGACAGGG	386		
QY	186	GACCCAGGCGCTGGCCCTCCATCCAGAAACCTATGACTCACCGCTACCTGGAGCAC	245		
DB	387	GACCCAGGCGCTGGCCCTCCATCCAGAAACCTATGACTCACCGCTACCTGGAGCAC	446		
QY	246	CRACTCCGAGCTTGGCTGGGACCTATCTGAATACCTGGGCCCCCTTTCAACGAGCCA	305		
DB	447	CRACTCCGAGCTTGGCTGGGACCTATCTGAATACCTGGGCCCCCTTTCAACGAGCCA	506		
QY	306	GACTTCAACCTCCCGCTGGGGGAGAGACTGCGCCAGGGCCACTGTGTGACTTGGAG	365		
DB	507	GACTTCAACCTCCCGCTGGGGGAGAGACTGCGCCAGGGCCACTGTGTGACTTGGAG	566		
QY	366	GTGTGGGGAAGCCTCAATGACAACTGCGGCTGACCCAGAACTACGAGGCTTACAGCCAC	425		
DB	567	GTGTGGGGAAGCCTCAATGACAACTGCGGCTGACCCAGAACTACGAGGCTTACAGCCAC	626		
QY	426	CTTCTGTGTACTGTGGTGGCTCAACCGTCAAGCTGCGCACTGCTGAGCTGCGCGCAGC	485		
DB	627	CTTCTGTGTACTGTGGTGGCTCAACCGTCAAGCTGCGCACTGCTGAGCTGCGCGCAGC	686		
QY	486	CTGGCCCACTTCTGCAACCAAGCTCCAGGGGCTGCTGGGCGAGCATTCGGGGCTCATGGCA	545		
DB	687	CTGGCCCACTTCTGCAACCAAGCTCCAGGGGCTGCTGGGCGAGCATTCGGGGCTCATGGCA	746		

QY	546	GCTCTGGGCTACCCACTGCCCCAGCCGCTGCTGGGACTGAACCCACTTTGGACTCCTGGC	605
DB	747	GCTCTGGGCTACCCACTGCCCCAGCCGCTGCTGGGACTGAACCCACTTTGGACTCCTGGC	806
QY	606	CCTGCCCAACAGTGACTTCTCCAGAGATGGAGACTTCTGGCTGCTGAAGAGCTGCAG	665
DB	807	CCTGCCCAACAGTGACTTCTCCAGAGATGGAGACTTCTGGCTGCTGAAGAGCTGCAG	866
QY	666	ACCTGGCTGTGGGCTGCGCCCAAGGACTTTCAACCGGCTCAAGAAGAGATGAGCCTCCA	725
DB	867	ACCTGGCTGTGGGCTGCGCCCAAGGACTTTCAACCGGCTCAAGAAGAGATGAGCCTCCA	926
QY	726	GCAGCTGCAGTCAACCTGTGCACCTGTGGGGGCTCATGGCTTCTGA	767
DB	927	GCAGCTGCAGTCAACCTGTGCACCTGTGGGGGCTCATGGCTTCTGA	968

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OM nucleic - nucleic search, using sw model

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SUMMARIES

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2	759.2	95.3	768	13	US-10-296-115-607
3	749.4	94.0	1710	15	US-10-212-793-1
4	669.4	84.0	819	9	US-09-931-704-4
5	668.4	83.9	968	13	US-10-276-774-916
6	523.4	65.7	5087	9	US-09-931-704-3
7	493.4	61.9	495	9	US-09-864-761-23175
8	369	46.3	492	9	US-09-864-761-6462
9	269.4	33.8	283	9	US-09-765-231A-75
10	175.8	22.1	809	13	US-10-027-632-134702
11	175.8	22.1	809	16	US-10-027-632-134702
12	80.2	10.1	395	15	US-10-212-793-7
13	58.6	7.4	65	10	US-09-908-975-29446
14	46.8	5.9	2320	13	US-09-925-298-266

Sequence 266, App	15	46.8	5.9	2320	15	US-10-102-806-266
Sequence 1, Appli	16	44.8	5.6	68750	14	US-10-014-717-1
Sequence 119, App	17	44	5.5	536	17	US-10-338-110-119
Sequence 143, App	18	43.6	5.5	3195	15	US-10-205-823-143
Sequence 54, Appl	19	43.6	5.5	3195	15	US-10-285-976-54
Sequence 127, Ap	20	43.6	5.5	3195	16	US-10-235-027-1127
Sequence 18, Appl	21	42	5.3	2085	17	US-10-311-623-18
Sequence 494, App	22	42	5.3	2771	13	US-10-112-944-494
Sequence 6, Appli	23	42	5.3	3206	13	US-10-112-944-6
Sequence 10, Appl	24	41.8	5.2	594	13	US-10-142-426-10
Sequence 10, Appl	25	41.8	5.2	594	15	US-10-123-155-10
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Sequence 10, Appl	34	41.8	5.2	594	16	US-10-141-759-10
Sequence 10, Appl	35	41.8	5.2	594	16	US-10-140-864-10
Sequence 10, Appl	36	41.8	5.2	594	16	US-10-140-864-10
Sequence 176, App	37	40.8	5.1	1581	16	US-10-369-493-43081
Sequence 176, App	38	40.8	5.1	980	15	US-10-175-523-176
Sequence 119, App	39	40.6	5.1	536	17	US-10-338-110-119
Sequence 3132, Ap	40	40.4	5.1	1083	15	US-10-156-761-3132
Sequence 1, Appli	41	40.4	5.1	9025608	15	US-10-156-761-1
Sequence 59, Appl	42	40.2	5.0	586	15	US-10-008-063-1
Sequence 983, App	43	40.2	5.0	586	15	US-10-152-363A-59
Sequence 4, Appli	44	40.2	5.0	690	13	US-10-087-192-983
	45	40.2	5.0	903	12	US-10-380-703-4

ALIGNMENTS

RESULT 1

US-09-931-704-1

; Sequence 1, Application US/09931704

; Patent No. US20020041873A1

; GENERAL INFORMATION:

; APPLICANT: Senaldi,

; TITLE OF INVENTION: Methods and Compositions for Treating IgE-Related Disease Using N

; TITLE OF INVENTION: Inhibitors

; FILE REFERENCE: A-695

; CURRENT APPLICATION NUMBER: US/09/931,704

; CURRENT FILING DATE: 2001-08-16

; PRIOR APPLICATION NUMBER: US 60/226,436

; PRIOR FILING DATE: 2000-08-18

; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1

; LENGTH: 797

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (90)..(764)

; OTHER INFORMATION:

; NAME/KEY: mac_peptide

; LOCATION: (171)..()

; OTHER INFORMATION: Met at -27

US-09-931-704-1

Query Match 100.0%; Score 797; DB 9; Length 797;

Best Local Similarity 100.0%; Pred. No. 5.4e-208; Mismatches 0; Indels 0; Gaps 0;

Matches 797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATTAAGCTTCGCCGAGCGCGGCTCCGCTCCACCTCCGACGCTCCGCGAGAGAG 60

1 ATTAAGCTTCGCCGAGCGCGGCTCCGCTCCACCTCCGACGCTCCGCGAGAGAG 60

Db 1 ATTAAGCTTCGCCGAGCGCGGCTCCGCTCCACCTCCGACGCTCCGCGAGAGAG 60

QY 61 CGCAGCCCGCGCGCCGCCACCCACCTCCGAGCGGGGACTCGTGGGGA 120

QY 540 ATGGCAGCTCTGGGTACCTACCTGCCCCAGCCGCTGCTGGAGTGAACCCACTTGGACT 599
Db 545 ATGGCAGCTCTGGGTACCTACCTGCCCCAGCCGCTGCTGGAGTGAACCCACTTGGACT 604
QY 600 CTGGCCCTGCCCCAGTGAATCTCTCCAGAGATGGAGTGAATCTCTGGCTCTCAAGGAG 659
Db 605 CTGGCCCTGCCCCAGTGAATCTCTCCAGAGATGGAGTGAATCTCTGGCTCTCAAGGAG 664
QY 660 CTGCAGACCTGGCTCTGGCGCTCGCCCAAGGACTTCAACCGGCTCAAGAGAGATGCAG 719
Db 665 CTGCAGACCTGGCTCTGGCGCTCGCCCAAGGACTTCAACCGGCTCAAGAGAGATGCAG 724
QY 720 CTTCAGCAGCTGAGTCACTGACCTGAGCTGGGGCTCATGGCTTCTGACCTTCTGACCTT 778
Db 725 CTTCAGCAGCTGAGTCACTGACCTGAGCTGGGGCTCATGGCTTCTGACCTTCTGACCTT 783

RESULT 5
US-10-276-774-916
; Sequence 916, Application US/10276774
; Publication No. US20040053245A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang, Y, Tom et al
; TITLE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-030
; CURRENT APPLICATION NUMBER: US/10/276,774
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 2700
; SOFTWARE: Custom
; SEQ ID NO 916
; LENGTH: 968
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-276-774-916

Query Match 83.9%; Score 668.4; DB 13; Length 968;
Best Local Similarity 97.0%; Pred. No. 7.6e-173;
Matches 681; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 66 CCGCGCCGCCAGCCAGCCGCCATGGACCTCCGAGCAGGGGACTCGTGGGGATGTTA 125
Db 267 CCGCGCCGCCAGCCAGCCGCCATGGACCTCCGAGCAGGGGACTCGTGGGGATGTTA 326
QY 126 GGGTGGCTGTGACCGGTCTGTGGGACCTCTCCAGAGATGGAGTGAATCTCTGGCTCTCAAGGAG 185
Db 327 GGGTGGCTGTGACCGGTCTGTGGGACCTCTCCAGAGATGGAGTGAATCTCTGGCTCTCAAGGAG 386
QY 186 GACCCAGGCGTGGCGCTCCATCCAGAGAACTATGACCTCACCGGCTACTCTGAGGAC 245
Db 387 GACCCAGGCGTGGCGCTCCATCCAGAGAACTATGACCTCACCGGCTACTCTGAGGAC 446
QY 246 CAACTCCGAGCTGTGGCTGGGACCTATCTGAATCTACTCTGGGCGCCCTTTCAACAGGCA 305
Db 447 CAACTCCGAGCTGTGGCTGGGACCTATCTGAATCTACTCTGGGCGCCCTTTCAACAGGCA 506
QY 306 GACTTCAACCTCCCGCTGGGGGAGAGACTCTGCCCAGGGCCACTGTTGACTTGGAG 365
Db 507 GACTTCAACCTCCCGCTGGGGGAGAGACTCTGCCCAGGGCCACTGTTGACTTGGAG 566
QY 366 GTGTGCGAGGCTCAATGACAACTGCGGCTGACCCAGAACTACAGGCTTACAGCCAC 425
Db 567 GTGTGCGAGGCTCAATGACAACTGCGGCTGACCCAGAACTACAGGCTTACAGCCAC 626
QY 426 CTCTGTGTACTTGGTGGCTCAACCTGAGGCTGACCTGAGCTGGCGCGGAGC 485
Db 627 CTCTGTGTACTTGGTGGCTCAACCTGAGGCTGACCTGAGCTGGCGCGGAGC 686

QY 486 CTGGCCCACTTCTGACACAGCCCTCAGGGCCTGCTGGGAGCATTTGCGGGCTCATGGCA 545
Db 687 CTGGCCCACTTCTGACACAGCCCTCAGGGCCTGCTGGGAGCATTTGCGGGCTCATGGCA 746
QY 546 GCTCTGGGCTACCCACTGCCCCAGCCGCTGCTGGGACTGAACCCACTTGGACTCTCTGGC 605
Db 747 GCTCTGGGCTACCCACTGCCCCAGCCGCTGCTGGGACTGAACCCACTTGGACTCTCTGGC 806
QY 606 CTTGCCCAAGTGAATCTCTCCAGAGATGGAGTGAATCTCTGGCTCTGAAGGAGTGCAG 665
Db 807 CTTGCCCAAGTGAATCTCTCCAGAGATGGAGTGAATCTCTGGCTCTGAAGGAGTGCAG 866
QY 666 ACCTGGCTGTGGCGCTCGGCCAAGGACTTCAACCGGCTCAAGAGAGATGCAGCTCA 725
Db 867 ACCTGGCTGTGGCGCTCGGCCAAGGACTTCAACCGGCTCAAGAGAGATGCAGCTCA 926
QY 726 GAGCTGCACTGACCTGACCTGAGGCTCATGGCTTCTGA 767
Db 927 GAGCTGCACTGACCTGACCTGAGGCTCATGGCTTCTGA 968

RESULT 6
US-09-931-704-3
; Sequence 3, Application US/09931704
; Patent No. US20020041873A1
; GENERAL INFORMATION:
; APPLICANT: Senaldi, Giorgio
; TITLE OF INVENTION: Methods and Compositions for Treating IgE-Related Disease Using N
; TITLE OF INVENTION: Inhibitors
; FILE REFERENCE: A-695
; CURRENT APPLICATION NUMBER: US/09/931,704
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: US 60/226,436
; PRIOR FILING DATE: 2000-08-18
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 3
; LENGTH: 5087
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; LOCATION: (137)..(138)
; OTHER INFORMATION: product = "INTERVENING UNSEQUENCED REGION OF >1KB"
US-09-931-704-3

Query Match 65.7%; Score 523.4; DB 9; Length 5087;
Best Local Similarity 99.8%; Pred. No. 3.7e-133;
Matches 524; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 271 ATCTGACTACTGGGGCCCCCTTCAACGAGCCAGACTTCAACCCCTCCCGGCTGGGG 330
Db 3363 AGCTGACTACTGGGGCCCCCTTCAACGAGCCAGACTTCAACCCCTCCCGGCTGGGG 3422
QY 331 CAGAGACTCTGCCAGGCGCCACTGTTGACTTGGAGTGGGAGAGCTCAATGACAAAC 390
Db 3423 CAGAGACTCTGCCAGGCGCCACTGTTGACTTGGAGTGGGAGAGCTCAATGACAAAC 3482
QY 391 TGGGGCTGACCCAGAACTAGAGGCTTACAGCCACTTCTGTGTACTTGGCTGGGCTCA 450
Db 3483 TGGGGCTGACCCAGAACTAGAGGCTTACAGCCACTTCTGTGTACTTGGCTGGGCTCA 3542
QY 451 ACCGTGAGGCTGACCTGCTGAGCTGCGCGCAGCTGCGCCACTTCTGACAGGCTCC 510
Db 3543 ACCGTGAGGCTGACCTGCTGAGCTGCGCGCAGCTGCGCCACTTCTGACAGGCTCC 3602
QY 511 AGGGCTGCTGGGAGCAGATTCGGGGCTGATGGAGCTTGGGCTACCCACTGCCCCAGC 570
Db 3603 AGGGCTGCTGGGAGCAGATTCGGGGCTGATGGAGCTTGGGCTACCCACTGCCCCAGC 3662
QY 571 CGTGTGCTGGGACTGAACCCACTTGGAGCTCTGGGCTTCCCAAGTGAATCTCTCCAGA 630
Db 3663 CGTGTGCTGGGACTGAACCCACTTGGAGCTCTGGGCTTCCCAAGTGAATCTCTCCAGA 3722

;; PRIOR FILING DATE: 2000-02-24
;; PRIOR APPLICATION NUMBER: US 60/167,363
;; PRIOR FILING DATE: 1999-11-23
;; PRIOR APPLICATION NUMBER: US 60/156,358
;; PRIOR FILING DATE: 1999-09-28
;; PRIOR APPLICATION NUMBER: US 60/146,002
;; PRIOR FILING DATE: 1999-08-09
;; NUMBER OF SEQ ID NOS: 325720
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 134702
;; LENGTH: 809
;; TYPE: DNA
;; ORGANISM: Human
US-10-027-632-134702

Query Match 22.1%; Score 175.8; DB 13; Length 809;
Best Local Similarity 86.9%; Pred. No. 3.2e-38;
Matches 192; Conservative 1; Mismatches 28; Indels 0; Gaps 0;

QY 66 CCCGGCGCGCCAGCCCGCCAGCCCATGACCTCCGAGCAGGGGACTCGTGGGGGATGTTA 125
DB 17 CCCGGCGCGCGCTCATGCTTCCTGTCATCTCGCCACAGGGGACTCGTGGGGGATGTTA 76
QY 126 GCGTGCCTGTGCACGGTGTCTCTGGCAGCTCCCTGCGAGTGCAGTGCACAGGG 185
DB 77 GCGTGCCTGTGCACGGTGTCTCTGGCAGCTCCCTGCGAGTGCAGTGCACAGGG 136
QY 186 GACCCAGGGCGCTGGCCCTCCATCCAGAAAACCTATGACCTACCGGCTACCTGGAGCAC 245
DB 137 GACCCAGGGCGCGCCCGCCCTCCATCCAGAAAACCTATGACCTACCGGCTACCTGGAGCAC 196
QY 246 CAACTCCGAGCTTGGCTGGGACCTATCTGAATACCTGGG 286
DB 197 CAACTCCGAGCTTGGCTGGGACCTATGTGAGTATCCAGCG 237

RESULT 11

US-10-027-632-134702
;; Sequence 134702, Application US/10027632
;; Publication No. US20030204075A9
;; GENERAL INFORMATION:
;; APPLICANT: Wang, David G.
;; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;; POLYMORPHISMS IN THE HUMAN GENOME
;; FILE REFERENCE: 108827.129
;; CURRENT APPLICATION NUMBER: US/10/027.632
;; PRIOR FILING DATE: 2002-04-30
;; PRIOR APPLICATION NUMBER: US 60/218,006
;; PRIOR FILING DATE: 2000-07-12
;; PRIOR APPLICATION NUMBER: US 60/198,676
;; PRIOR FILING DATE: 2000-04-20
;; PRIOR APPLICATION NUMBER: US 60/193,483
;; PRIOR FILING DATE: 2000-03-29
;; PRIOR APPLICATION NUMBER: US 60/185,218
;; PRIOR FILING DATE: 2000-02-24
;; PRIOR APPLICATION NUMBER: US 60/167,363
;; PRIOR FILING DATE: 1999-11-23
;; PRIOR APPLICATION NUMBER: US 60/156,358
;; PRIOR FILING DATE: 1999-09-28
;; PRIOR APPLICATION NUMBER: US 60/146,002
;; PRIOR FILING DATE: 1999-08-09
;; NUMBER OF SEQ ID NOS: 325720
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 134702
;; LENGTH: 809
;; TYPE: DNA
;; ORGANISM: Human
US-10-027-632-134702

Query Match 22.1%; Score 175.8; DB 16; Length 809;
Best Local Similarity 86.9%; Pred. No. 3.2e-38;
Matches 192; Conservative 1; Mismatches 28; Indels 0; Gaps 0;

QY 66 CCCGGCGCGCCAGCCCGCCAGCCCATGACCTCCGAGCAGGGGACTCGTGGGGGATGTTA 125
DB 17 CCCGGCGCGCGCTCATGCTTCCTGTCATCTCGCCACAGGGGACTCGTGGGGGATGTTA 76
QY 126 GCGTGCCTGTGCACGGTGTCTCTGGCAGCTCCCTGCGAGTGCAGTGCACAGGG 185
DB 77 GCGTGCCTGTGCACGGTGTCTCTGGCAGCTCCCTGCGAGTGCAGTGCACAGGG 136
QY 186 GACCCAGGGCGCTGGCCCTCCATCCAGAAAACCTATGACCTACCGGCTACCTGGAGCAC 245
DB 137 GACCCAGGGCGCGCCCGCCCTCCATCCAGAAAACCTATGACCTACCGGCTACCTGGAGCAC 196
QY 246 CAACTCCGAGCTTGGCTGGGACCTATCTGAATACCTGGG 286
DB 197 CAACTCCGAGCTTGGCTGGGACCTATGTGAGTATCCAGCG 237

RESULT 12
US-10-212-793-7
;; Sequence 7, Application US/10212793
;; Publication No. US20030087395A1
;; GENERAL INFORMATION:
;; APPLICANT: Shi et al.
;; TITLE OF INVENTION: Cardiotrophin-Like Cytokine
;; FILE REFERENCE: PF385D1C1
;; CURRENT APPLICATION NUMBER: US/10/212,793
;; CURRENT FILING DATE: 2002-08-07
;; PRIOR APPLICATION NUMBER: US 09/438,299
;; PRIOR FILING DATE: 1999-11-12
;; PRIOR APPLICATION NUMBER: US 09/106,182
;; PRIOR FILING DATE: 1998-06-29
;; PRIOR APPLICATION NUMBER: US 60/051,311
;; PRIOR FILING DATE: 1997-06-30
;; NUMBER OF SEQ ID NOS: 24
;; SEQ ID NO 7
;; LENGTH: 396
;; TYPE: DNA
;; ORGANISM: homo sapiens
;; FEATURE:
;; NAME/KEY: Site
;; LOCATION: (199)
;; OTHER INFORMATION: n equals any nucleotide
;; FEATURE:
;; NAME/KEY: Site
;; LOCATION: (293)
;; OTHER INFORMATION: n equals any nucleotide
;; FEATURE:
;; NAME/KEY: Site
;; LOCATION: (306)
;; OTHER INFORMATION: n equals any nucleotide
;; FEATURE:
;; NAME/KEY: Site
;; LOCATION: (360)
;; OTHER INFORMATION: n equals any nucleotide
;; FEATURE:
;; NAME/KEY: Site
;; LOCATION: (371)
;; OTHER INFORMATION: n equals any nucleotide
;; FEATURE:
;; NAME/KEY: Site
;; LOCATION: (377)
;; OTHER INFORMATION: n equals any nucleotide
;; FEATURE:
;; NAME/KEY: Site
;; LOCATION: (383)
;; OTHER INFORMATION: n equals any nucleotide
US-10-212-793-7

Query Match 10.1%; Score 80.2; DB 15; Length 396;
Best Local Similarity 96.5%; Pred. No. 4.1e-12;
Matches 82; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 711 AAGATGCAGCCTCCAGCAGCTGCAGTCCACCTGCAGCTGGGGGCTCATGGCTTCTGACTT 770

QY 311 CAACCTCCCGCTGGGGGAGAGACTCTGCCCAGGG 348
| | | | | | | | | | | | | | | | | |
Db 364 CCACCTCCCGCTGGGGGATGGGACGATGCAGAGGG 401
| | | | | | | | | | | | | | | | | |

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Job time : 467.864 secs

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OM nucleic - nucleic search, using sw model

Run on: August 15, 2004, 16:10:45 ; Search time 58.7376 Seconds
(without alignments)
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Title: US-09-931-704-1
Perfect score: 797
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
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Listing first 45 summaries

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6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	797	100.0	797	1	US-08-792-019B-1
2	797	100.0	797	3	US-08-988-819-1
3	797	100.0	797	3	US-09-016-534-1
4	749.4	94.0	1710	3	US-09-106-182-1
5	669.4	84.0	819	3	US-08-792-019B-4
6	669.4	84.0	819	3	US-08-988-819-4
7	669.4	84.0	819	3	US-09-016-534-4
8	523.4	65.7	5087	1	US-08-792-019B-3
9	523.4	65.7	5087	3	US-08-988-819-3
10	523.4	65.7	5087	3	US-09-016-534-3
11	80.2	10.1	396	3	US-09-106-182-7
12	44.8	5.6	68750	3	US-09-335-409-1
13	44.8	5.6	68750	4	US-09-368-102-1
14	44.8	5.6	68750	4	US-09-567-969-1
15	44.8	5.6	68750	4	US-09-568-480-1
16	44.8	5.6	68750	4	US-09-568-486-1
17	44.8	5.6	68750	4	US-09-568-472-1
18	44.8	5.6	68750	4	US-09-567-899-1
19	42.2	5.3	1590	4	US-09-252-991A-10070
20	42.2	5.3	1878	4	US-09-252-991A-9765
21	39.6	5.0	430	4	US-09-621-976-16656
22	39	4.9	364	4	US-09-621-976-17202
23	38.6	4.8	364	4	US-09-621-976-17202
24	38.6	4.8	6858	4	US-09-252-991A-1219
25	38.4	4.8	71989	4	US-09-443-501A-2
26	38	4.8	223	1	US-08-383-761-1
27	38	4.8	223	1	US-08-824-277-1

C 28	37.8	4.7	3129	3	US-09-387-695-1	Sequence 1, Appli
C 29	37.8	4.7	49272	1	US-08-614-770A-1	Sequence 1, Appli
C 30	37.6	4.7	1071	4	US-09-252-991A-14206	Sequence 14206, A
C 31	37.6	4.7	2388	4	US-09-252-991A-14064	Sequence 14064, A
C 32	37.4	4.7	900	4	US-09-252-991A-9282	Sequence 9282, Ap
C 33	37.4	4.7	3729	4	US-09-252-991A-9272	Sequence 9272, Ap
C 34	37.2	4.7	1242	4	US-09-252-991A-9668	Sequence 9668, Ap
C 35	37.2	4.7	1521	4	US-09-252-991A-9746	Sequence 9746, Ap
C 36	37.2	4.7	2511	4	US-09-252-991A-9494	Sequence 9494, Ap
C 37	37.2	4.7	2583	4	US-09-252-991A-9541	Sequence 9541, Ap
C 38	37.2	4.7	3984	4	US-09-016-434-1199	Sequence 1199, Ap
C 39	37.2	4.7	4559	4	US-09-919-172-61	Sequence 61, Appl
C 40	37	4.6	468	4	US-09-252-991A-3528	Sequence 3528, Ap
C 41	37	4.6	1449	4	US-09-252-991A-3558	Sequence 3558, Ap
C 42	37	4.6	1698	4	US-09-252-991A-3551	Sequence 3551, Ap
C 43	37	4.6	2196	4	US-09-252-991A-3536	Sequence 3536, Ap
C 44	36.8	4.6	336	4	US-09-252-991A-12979	Sequence 12979, A
C 45	36.8	4.6	1059	4	US-09-252-991A-12662	Sequence 12662, A

ALIGNMENTS

RESULT 1
US-08-792-019B-1
; Sequence 1, Application US/08792019B
; Patent No. 5741772
; GENERAL INFORMATION:
; APPLICANT: CHANG, MING-SHI
; TITLE OF INVENTION: THE NEUROTROPHIC FACTOR NNT-1
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMGEN INC.
; STREET: 1840 DEHAVILLAND DRIVE
; CITY: THOUSAND OAKS
; STATE: CA
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/792.019B
; FILING DATE: 03-FEB-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: COOK, ROBERT R.
; REGISTRATION NUMBER: 31,602
; REFERENCE/DOCKET NUMBER: A-442
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 797 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 90..764
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 171..764
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 90..170
US-08-792-019B-1

Query Match 100.0%; Score 797; DB 1; Length 797;
Best Local Similarity 100.0%; Pred. No. 3.6e-189;
Matches 797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATTTAAAGCTTCCGCGAGCCGCGCTGCGCTCCCACTCCGCGAGCTCCGCGAGGAG 60
Db 1 ATTTAAAGCTTCCGCGAGCCGCGCTGCGCTCCCACTCCGCGAGCTCCGCGAGGAG 60
QY 61 CGCAGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
Db 61 CGCAGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
QY 121 TGTAGCGTGTGTCGACGCGTGTGTCGACGCGTGTGTCGACGCGTGTGTCG 180
Db 121 TGTAGCGTGTGTCGACGCGTGTGTCGACGCGTGTGTCGACGCGTGTGTCG 180
QY 181 CAGGGGACCCAGGGGCTGCGCGCTCCATCCAGAAACCTATGACTCACCCTACCTGG 240
Db 181 CAGGGGACCCAGGGGCTGCGCGCTCCATCCAGAAACCTATGACTCACCCTACCTGG 240
QY 241 AGCACCAACTCCGAGCTTGGCTGGGACCTATCTGAATACCTGGGCGCCCTTTCAAG 300
Db 241 AGCACCAACTCCGAGCTTGGCTGGGACCTATCTGAATACCTGGGCGCCCTTTCAAG 300
QY 301 AGCCAGACTTCAACCTCCCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
Db 301 AGCCAGACTTCAACCTCCCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
QY 421 GCCACCTTCTGTGTTACTTGGTGGGCTCAACCGTCAAGGCTGCGGCTGCG 480
Db 421 GCCACCTTCTGTGTTACTTGGTGGGCTCAACCGTCAAGGCTGCGGCTGCG 480
QY 481 GCAGCTTGGGCGGCTTCTGCAACGCGCTCCAGGCGCTGCGGCGCTGCGG 540
Db 481 GCAGCTTGGGCGGCTTCTGCAACGCGCTCCAGGCGCTGCGGCGCTGCGG 540
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RESULT 2
US-08-988-819-1
; Sequence 1, Application US/08988819
; Patent No. 6054294
; GENERAL INFORMATION:
; APPLICANT: CHANG, MING-SHI
; TITLE OF INVENTION: NEUROTROPHIC FACTOR NNT-1
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMGEN INC.
; STREET: ONE AMGEN CENTER DRIVE
; CITY: THOUSAND OAKS
; STATE: CA
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/988,819
; FILING DATE: 12-DEC-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/792,019
; FILING DATE: 03-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: COOK, ROBERT R.
; REGISTRATION NUMBER: 31,602
; REFERENCE/DOCKET NUMBER: A-442A
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 797 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 90..764
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 171..764
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 90..170
;
US-08-988-819-1

Query Match 100.0%; Score 797; DB 3; Length 797;
Best Local Similarity 100.0%; Pred. No. 3.6e-189;
Matches 797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATTTAAAGCTTCCGCGAGCCGCGCTGCGCTCCCACTCCGCGAGCTCCGCGAGGAG 60
Db 1 ATTTAAAGCTTCCGCGAGCCGCGCTGCGCTCCCACTCCGCGAGCTCCGCGAGGAG 60
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Db 61 CGCAGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
QY 121 TGTAGCGTGTGTCGACGCGTGTGTCGACGCGTGTGTCGACGCGTGTGTCG 180
Db 121 TGTAGCGTGTGTCGACGCGTGTGTCGACGCGTGTGTCGACGCGTGTGTCG 180
QY 181 CAGGGGACCCAGGGGCTGCGCGCTCCATCCAGAAACCTATGACTCACCCTACCTGG 240
Db 181 CAGGGGACCCAGGGGCTGCGCGCTCCATCCAGAAACCTATGACTCACCCTACCTGG 240
QY 241 AGCACCAACTCCGAGCTTGGCTGGGACCTATCTGAATACCTGGGCGCCCTTTCAAG 300
Db 241 AGCACCAACTCCGAGCTTGGCTGGGACCTATCTGAATACCTGGGCGCCCTTTCAAG 300
QY 301 AGCCAGACTTCAACCTCCCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
Db 301 AGCCAGACTTCAACCTCCCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
QY 361 TGGAGGTGTGGGAAAGCCTCAATGAAACTGGGCTGACCACTGCGGCTGCGG 420
Db 361 TGGAGGTGTGGGAAAGCCTCAATGAAACTGGGCTGACCACTGCGGCTGCGG 420
QY 421 GCCACCTTCTGTGTTACTTGGTGGGCTCAACCGTCAAGGCTGCGGCTGCG 480
Db 421 GCCACCTTCTGTGTTACTTGGTGGGCTCAACCGTCAAGGCTGCGGCTGCG 480
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QY 541 TGGGAGCTCTGGGCTACCCACTGCCCCAGCGCTGCTGGAGCTGAACCCACTTGGACTC 600
Db 541 TGGGAGCTCTGGGCTACCCACTGCCCCAGCGCTGCTGGAGCTGAACCCACTTGGACTC 600
QY 601 CTGGCCCTGCCACAGTACTTCTCCAGAAAGATGGAGACTTCTGGCTGCTGAAGAGC 660
Db 601 CTGGCCCTGCCACAGTACTTCTCCAGAAAGATGGAGACTTCTGGCTGCTGAAGAGC 660
QY 661 TGCAGACTGGCTGTGGCGCTCGGCCAAGGACTTCAACCGGCTCAAGAAGAGATGCAGC 720
Db 661 TGCAGACTGGCTGTGGCGCTCGGCCAAGGACTTCAACCGGCTCAAGAAGAGATGCAGC 720
QY 721 CTCAGAGCTGAGTACACCTGACCTGCGGGCTCATGGCTTCTGACTTCTGACCTTCT 780
Db 721 CTCAGAGCTGAGTACACCTGACCTGCGGGCTCATGGCTTCTGACTTCTGACCTTCT 780
QY 781 CCTCTTGGCTCCCCCCC 797
Db 781 CCTCTTGGCTCCCCCCC 797

RESULT 3

US-09-016-534-1
; Sequence 1, Application US/09016534
; Patent No. 6143874
; GENERAL INFORMATION:
; APPLICANT: CHANG, MING-SHI
; APPLICANT: ELLIOTT, GARY S.
; APPLICANT: SARMIENTO, ULLA
; APPLICANT: SENALDI, GIORGIO
; TITLE OF INVENTION: THE NEUROTROPHIC FACTOR NNT-1
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMGEN INC.
; STREET: ONE AMGEN CENTER
; CITY: THOUSAND OAKS
; STATE: CA
; COUNTRY: USA
; ZIP: 91320

COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,534
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/792,019
FILING DATE: 03-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: COOK, ROBERT R.
REGISTRATION NUMBER: 31,602
REFERENCE/DOCKET NUMBER: A-442B
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 797 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA

FEATURE:
NAME/KEY: CDS
LOCATION: 90..764
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 171..764
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 90..170
US-09-016-534-1

Query Match 100.0%; Score 797; DB 3; Length 797;
Best Local Similarity 100.0%; Pred No. 3,6e-189; Indels 0; Gaps 0;
Matches 797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATTAAGACTTTCGCGAGCGCGGCTCGCCCTCCCACTCCGACAGCTCCGGAGAGGAG 60
Db 1 ATTAAGACTTTCGCGAGCGCGGCTCGCCCTCCCACTCCGACAGCTCCGGAGAGGAG 60
QY 61 CCGCAGCCCGCGCGCCAGCCCGCCAGCCCATCGACCTCCGAGCAGGGGACTCGTGGGGGA 120
Db 61 CCGCAGCCCGCGCGCCAGCCCGCCAGCCCATCGACCTCCGAGCAGGGGACTCGTGGGGGA 120
QY 121 TGTAGCGTCCCTGTGTGACAGCGTCTCTGGCACTCCCTGCACTGCGCAGCTCTCAATCGCA 180
Db 121 TGTAGCGTCCCTGTGTGACAGCGTCTCTGGCACTCCCTGCACTGCGCAGCTCTCAATCGCA 180
QY 181 CAGGGAGCCAGCGGCTGCGCCCTCCATCCAGAAACCTATGACCTCACCCGCTACCTGG 240
Db 181 CAGGGAGCCAGCGGCTGCGCCCTCCATCCAGAAACCTATGACCTCACCCGCTACCTGG 240
QY 241 AGCAGCAACTCCGAGCTTGGCTGGGACCTATCTGAACCTACCTGGGCCCCCTTTCAACG 300
Db 241 AGCAGCAACTCCGAGCTTGGCTGGGACCTATCTGAACCTACCTGGGCCCCCTTTCAACG 300
QY 301 AGCCAGACTTCAACCTTCCCGCTGGGGGAGAGACTCTGCCCGAGGGGCACTGTGTGACT 360
Db 301 AGCCAGACTTCAACCTTCCCGCTGGGGGAGAGACTCTGCCCGAGGGGCACTGTGTGACT 360
QY 361 TGGAGGTGGCGAAGCCCTCAATGACAACTCCGGCTGACCCAGAACTACGAGGGCTTACA 420
Db 361 TGGAGGTGGCGAAGCCCTCAATGACAACTCCGGCTGACCCAGAACTACGAGGGCTTACA 420
QY 421 GGCACCTTCTGTGTACTTGTGCTGCTGCTCAACCGTCAAGCTGCTGAGCTGCGCC 480
Db 421 GGCACCTTCTGTGTACTTGTGCTGCTCAACCGTCAAGCTGCTGAGCTGCGCC 480
QY 481 GCAGCTGGCCCACTTCTGCACAGCCCTCCAGGGGCTGCTGGGAGCATTGGGGGCTCA 540
Db 481 GCAGCTGGCCCACTTCTGCACAGCCCTCCAGGGGCTGCTGGGAGCATTGGGGGCTCA 540
QY 541 TGGCAGCTCTGGGCTACCCACTGCCCCAGCGCTGCTGGGACTGAACCCACTTGGACTC 600
Db 541 TGGCAGCTCTGGGCTACCCACTGCCCCAGCGCTGCTGGGACTGAACCCACTTGGACTC 600
QY 601 CTGGCCCTGCCACAGTACTTCTCCAGAAAGATGGAGACTTCTGGCTGCTGAAGAGC 660
Db 601 CTGGCCCTGCCACAGTACTTCTCCAGAAAGATGGAGACTTCTGGCTGCTGAAGAGC 660
QY 661 TGCAGACTGGCTGTGGCGCTCGGCCAAGGACTTCAACCGGCTCAAGAAGAGATGCAGC 720
Db 661 TGCAGACTGGCTGTGGCGCTCGGCCAAGGACTTCAACCGGCTCAAGAAGAGATGCAGC 720
QY 721 CTCAGAGCTGAGTACACCTGACCTGCGGGCTCATGGCTTCTGACTTCTGACCTTCT 780
Db 721 CTCAGAGCTGAGTACACCTGACCTGCGGGCTCATGGCTTCTGACTTCTGACCTTCT 780
QY 781 CCTCTTGGCTCCCCCCC 797
Db 781 CCTCTTGGCTCCCCCCC 797

RESULT 4

US-09-106-182-1
; Sequence 1, Application US/09106182
; Patent No. 6046035
; GENERAL INFORMATION:
; APPLICANT: Shi, Yangu
; APPLICANT: Ruben, Steve
; TITLE OF INVENTION: Cardiotrophin-Like Cytokine
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc
; STREET: 9410 Key West Ave

CITY: Rockville
STATE: MD
COUNTRY: US
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/106.182
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/051,053
FILING DATE: 30-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Brookes A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: P385
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1710 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 46..720
NAME/KEY: sig_peptide
LOCATION: 46..126
NAME/KEY: mat_peptide
LOCATION: 127..720
US-09-106-182-1
Query Match 94.0%; Score 749.4; DB 3; Length 1710;
Best Local Similarity 99.9%; Pred. No. 3e-177;
Matches 750; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 45 GCCTCGGAGAGGAGCCGACCCCGCGCCGAGCCCGCCAGCCCATGGACCTCCGAGCA 104
DB 1 GCCTCGGAGAGGAGCCGACCCCGCGCCGAGCCCGCCAGCCCATGGACCTCCGAGCA 60
QY 105 GGGGACTCTGGGGGATGTTAGCGTGTGTCAGCGTGTCTGGACCTCCCTGCAGTG 164
DB 61 GGGGACTCTGGGGGATGTTAGCGTGTGTCAGCGTGTCTGGACCTCCCTGCAGTG 120
QY 165 CAGCTCTCAATCGACAGGGGACCCAGGCGCTGCCCTCCATCCAGAAACCTATGAC 224
DB 121 CAGCTCTCAATCGACAGGGGACCCAGGCGCTGCCCTCCATCCAGAAACCTATGAC 180
QY 225 CTCACCCGCTACTCGGAGCACCACCTCCGAGCTTGGCTGGGACCTATCTGAATACCTG 284
DB 181 CTCACCCGCTACTCGGAGCACCACCTCCGAGCTTGGCTGGGACCTATCTGAATACCTG 240
QY 285 GGGCCCTTTTAAAGAGCAGACTTCAACCTCCCGCGCTGGGGCAGAGACTCGGCC 344
DB 241 GGGCCCTTTTAAAGAGCAGACTTCAACCTCCCGCGCTGGGGCAGAGACTCGGCC 300
QY 345 AGGGCCACTTGTACCTTGGAGGTGGCGAAGCCTCAATGACAAATCGGGCTGACCCAG 404
DB 301 AGGGCCACTTGTACCTTGGAGGTGGCGAAGCCTCAATGACAAATCGGGCTGACCCAG 360
QY 405 AACTAGAGGCGCTACAGCCACCTTCTGTGTACTTCGGTGGGCTCAACCGTCAGGCTGCC 464
DB 361 AACTAGAGGCGCTACAGCCACCTTCTGTGTACTTCGGTGGGCTCAACCGTCAGGCTGCC 420

1465 ACTGCTGAGCTGGCGGCGAGCTGCGCCACCTTCTGACAGGCTCCAGGCGCTGCTGGGC 524
1421 ACTGCTGAGCTGGCGGCGAGCTGCGCCACCTTCTGACAGGCTCCAGGCGCTGCTGGGC 480
1525 AGCAATTGCGGGCGTCAATGCGAGCTCTGGGCTACCCACTGCCCCAGCCGCTGCTGGGACT 584
1481 AGCAATTGCGGGCGTCAATGCGAGCTCTGGGCTACCCACTGCCCCAGCCGCTGCTGGGACT 540
1585 GAACCCACTTGGACTCTGCTGGCCCTGCCACAGTGACTTCTCCAGAAATGAGACGACTTC 644
1541 GAACCCACTTGGACTCTGCTGGCCCTGCCACAGTGACTTCTCCAGAAATGAGACGACTTC 600
1645 TGGCTGCTGAAGGAGCTGCGAGACCTGCGTGTGTCGCGCTCGGCCAAGGACTTCAACCGGCTC 704
1601 TGGCTGCTGAAGGAGCTGCGAGACCTGCGTGTGTCGCGCTCGGCCAAGGACTTCAACCGGCTC 660
1705 AAGAGAAGATGCGAGCTCCAGAGCTGCGAGTGCAGTGCAGCTGGGGGCTCATGGCTTC 764
1661 AAGAGAAGATGCGAGCTCCAGAGCTGCGAGTGCAGTGCAGCTGGGGGCTCATGGCTTC 720
1765 TGACTTCTGACCTTCT 795
1721 TGACTTCTGACCTTCT 751

RESULT 5
US-08-792-019B-4
; Sequence 4, Application US/08792019B
; Patent No. 5741772
; GENERAL INFORMATION:
; APPLICANT: CHANG, MING-SHI
; TITLE OF INVENTION: THE NEUROTROPHIC FACTOR NNT-1
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMGEN INC.
; STREET: 1840 DEHAVILLAND DRIVE
; CITY: THOUSAND OAKS
; STATE: CA
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/792,019B
; FILING DATE: 03-FEB-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: COOK, ROBERT R.
; REGISTRATION NUMBER: 31,602
; REFERENCE/DOCKET NUMBER: A-442
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 819 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 95..769
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 176..769
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 95..175
US-08-792-019B-4
Query Match 84.0%; Score 669.4; DB 1; Length 819;
Best Local Similarity 92.0%; Pred. No. 1.9e-157;

Db 545 ATGGGAGCTTGGCTACCCACTGCCCCAGGCTCTGCGAGGAGTGAAGCCAGCTGGGCC 604
Qy 600 CTGGCCCTTGGCCACAGTACTTCTCCAGAGATGAGGACTTCTGGCTGCTGAAGGAG 659
Db 605 CTGGCCCTTGGCCACAGTACTTCTCCAGAGATGAGGACTTCTGGCTGCTGAAGGAG 664
Qy 660 CTGGAGACTGCTGGCTGGCTGGCCAGGACTTCAACGGCTCAAGAGAGATGAG 719
Db 665 CTGGAGACTGCTGGCTGGCTGGCCAGGACTTCAACGGCTTAAAGAGAGATGAG 724
Qy 720 CTCCAGAGCTGAGTCAACCTGACCTGGGGCTCATGGCTTCTGACTTCTGACTT 778
Db 725 CTCCAGAGCTTGAATCACTGCTGACTTGGAGGACATGTTCTGACCTCTGACCT 783

RESULT 7
US-09-016-534-4
; Sequence 4, Application US/09016534
; Patent No. 6143874
; GENERAL INFORMATION:
; APPLICANT: CHANG, MING-SHI
; APPLICANT: ELLIOTT, GARY S.
; APPLICANT: SARMIENTO, ULLA
; APPLICANT: SENALI, GIORGIO
; TITLE OF INVENTION: THE NEUROTROPHIC FACTOR NNT-1
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMGEN INC.
; STREET: ONE AMGEN CENTER
; CITY: THOUSAND OAKS
; STATE: CA
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,534
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/792,019
; FILING DATE: 03-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: COOK, ROBERT R.
; REGISTRATION NUMBER: 31,602
; REFERENCE/DOCKET NUMBER: A-442B
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 819 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 95..769
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 176..769
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 95..175
; US-09-016-534-4
Query Match 84.0%; Score 669.4; DB 3; Length 819;
Best Local Similarity 92.0%; Pred. No. 1.9e-157;
Matches 717; Conservative 0; Mismatches 61; Indels 1; Gaps 1;
Qy 1 ATTAAGCTTGGCGAGCGGGCTCGCCCTCCCACTCCGCGAGGCTCCGCGAGGAG 60

Db 5 ATTAAGCTTCCGCGAGCGGGCTCGCCCTCCCACTCCGCGAGGCTCTGGGAGAGGAG 64
Qy 61 CCGACCCCGCGCGCCAG-CCCCAGCCCCATGGACCTCCGAGAGGAGGACTCTGGGGG 119
Db 65 CCGCGCCCGCGCGCGCGCGCCAGCCCCATGGACCTCCGAGAGGAGGACTCTGGGGG 124
Qy 120 ATGTTAGCTGCTGTGACACGGTGTCTGGCACTTCCCTGCACTGAGTGCAGCTCTCAATGC 179
Db 125 ATGTTAGCTGCTGTATGACAGGCTGTGTGGCACTTCCCTGCACTGAGTGCAGCTCTCAATGC 184
Qy 180 ACAGGGGACCGAGGGCTGGCCCTCCATTCAGAGAAAACCTATGACCTCAACCGCTACCTG 239
Db 185 ACAGGAGATCCAGGGCTGGCCCTCCATTCAGAGAAAACCTATGACCTCAACCGCTACCTG 244
Qy 240 GAGCACCAGCTCCGAGCTTGGCTGGGACTTATCTGAACCTAGCTGGGCCCCCTTTCAAC 299
Db 245 GAGCATCAACTCCGAGCTTAGCTGGGACTTACTTGAACCTAGCTGGGCCCCCTTTCAAC 304
Qy 300 GAGCCAGACTTCAACCTCCCGCTGGGGGAGAGACTTCTGCCAGGGCCACTGTTGAC 359
Db 305 GAGCCTGACTTCAATCTCTCGACTGGGGGAGAGAACTCTGCCAGGGCCACTGTTGAC 364
Qy 360 TTGGAGCTGTGGGAGAGCTCAATGACAACTGCGGCTGACCCAGAACTACGAGGCTAC 419
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Qy 420 AGCCAGCTTCTGTGTACTTGGCTGGGCTCAACCGCTCAGGCTGCCACTGCTGAGCTGCGC 479
Db 425 AGTCACCTCTGTGTACTTGGCTGGGCTCAACCGCTCAGGCTGCCACTGAACTCCGA 484
Qy 480 CGAGGCTGGCCCACTTCTGACAGGCTCCAGGGCTGCTGGGAGGACTTGGGGGCTC 539
Db 485 CGTAGCTGGCCCACTTCTGACAGGCTCCAGGGCTGCTGGGAGGACTTGGAGGTGC 544
Qy 540 ATGGCAGCTCTGGGCTTACCCACTGCCCCAGCGGCTGCTGGGAGTGAACCCACTTGGACT 599
Db 545 ATGGCAGCTTGGCTTACCCACTGCCCCAGCGCTGCTGGGAGGACTTGGGGCTGGGCC 604
Qy 600 CTGGGCTGGCCCACTGCTTCTCCAGAGATGAGGAGCTTCTGGCTGCTGAAGGAG 659
Db 605 CTGGGCTGGCCCACTGCTTCTCCAGAGATGAGGAGCTTCTGGCTGCTGAAGGAG 664
Qy 660 CTGCAGACTGCTGTGGGCTCGGGCTCGGCAAGGACTTCAACCGGCTCAAGAGAGATGACAG 719
Db 665 CTGCAGACTGCTGTGGCTTGGGCTTCCAGAGGACTTCAACCGGCTTAAAGAGAGATGACAG 724
Qy 720 CTCCAGAGCTGCACTCACTGACCTGACCTGGGGCTCATGGCTTCTGACTTCTGACTT 778
Db 725 CTCCAGAGCTTCACTCACTGACCTGCACTGGAGGCACTGGTTTCTGACCTCTGACCT 783

RESULT 8
US-08-792-019B-3
; Sequence 3, Application US/08792019B
; Patent No. 5741772
; GENERAL INFORMATION:
; APPLICANT: CHANG, MING-SHI
; TITLE OF INVENTION: THE NEUROTROPHIC FACTOR NNT-1
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMGEN INC.
; STREET: 1840 DEHAVILLAND DRIVE
; CITY: THOUSAND OAKS
; STATE: CA
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/792,019B

;; FILING DATE: 03-FEB-1997
;; CLASSIFICATION: 514
;; ATTORNEY/AGENT INFORMATION:
;; NAME: COOK, ROBERT R.
;; REGISTRATION NUMBER: 31,602
;; REFERENCE/DOCKET NUMBER: A-442
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 5087 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: 137..138
;; OTHER INFORMATION: /product= "INTERVENING UNSEQUENCED"
;; OTHER INFORMATION: REGION OF >1KB"
US-08-792-019B-3

Query Match 65.7%; Score 523.4; DB 1; Length 5087;
Best Local Similarity 99.8%; Pred. No. 6.2e-121;
Matches 524; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 271 ATCTGAACCTACTGGGCCCCCTTTCAACGAGCCAGACTTCAACCCCTCCCGCTGGGG 330
Db |||||
QY 3363 AGCTGAACCTACTGGGCCCCCTTTCAACGAGCCAGACTTCAACCCCTCCCGCTGGGG 3422
Db |||||
QY 331 CAGAGACTCTGCCAGGCCCCCTTTGACTTGGAGGTGTGGCGAAGCCTCAATGACAAAC 390
Db |||||
QY 3423 CAGAGACTCTGCCAGGCCCCCTTTGACTTGGAGGTGTGGCGAAGCCTCAATGACAAAC 3482
Db |||||
QY 391 TGGCGCTGACCCAGAGACTACGAGCCCTACAGCCACCTTCTGTACTTGGTGGCCTCA 450
Db |||||
QY 3483 TGGCGCTGACCCAGAGACTACGAGCCCTACAGCCACCTTCTGTACTTGGTGGCCTCA 3542
Db |||||
QY 451 ACCGTGAGCTGACCCAGAGACTACGAGCCCTACAGCCACCTTCTGTACTTGGTGGCCTCA 510
Db |||||
QY 3543 ACCGTGAGCTGACCCAGAGACTACGAGCCCTACAGCCACCTTCTGTACTTGGTGGCCTCA 3602
Db |||||
QY 511 AGGGCTCTGGGAGAGATTGGGGCGTCAATGGAGCTTGGGCTACCCACTGCCCCAGC 570
Db |||||
QY 3603 AGGGCTCTGGGAGAGATTGGGGCGTCAATGGAGCTTGGGCTACCCACTGCCCCAGC 3662
Db |||||
QY 571 CGCTGCTGGGAGCTGACCCAGAGACTACGAGCCCTACAGCCACCTTCTGTACTTGGTGGCCTCA 630
Db |||||
QY 3663 CGCTGCTGGGAGCTGACCCAGAGACTACGAGCCCTACAGCCACCTTCTGTACTTGGTGGCCTCA 3722
Db |||||
QY 631 AGATGGAGCTTCTGGCTGTGAAGGAGCTGACAGCTTGGCTGTGGCGCTCGGCCAAG 690
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QY 691 ACTTCAACCGGCTCAAGAGAGATGAGCCTTCCAGCAGCTGACGTACCCCTGCACTGG 750
Db |||||
QY 3783 ACTTCAACCGGCTCAAGAGAGATGAGCCTTCCAGCAGCTGACGTACCCCTGCACTGG 3842
Db |||||
QY 751 GGGCTCATGGCTTCTGACTTCTGACTTCTGACTTCTGCTTCTGCTCCCC 795
Db |||||
QY 3843 GGGCTCATGGCTTCTGACTTCTGACTTCTGACTTCTGCTTCTGCTCCCC 3887
Db |||||

RESULT 9
US-08-988-819-3
; Sequence 3, Application US/08988819
; Patent No. 6054294
; GENERAL INFORMATION:
; APPLICANT: CHANG, MING-SHI
; TITLE OF INVENTION: NEUROTROPIC FACTOR NNT-1
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMGEN INC.
; STREET: ONE AMGEN CENTER DRIVE
; CITY: THOUSAND OAKS

;; STATE: CA
;; COUNTRY: USA
;; ZIP: 91320
;; COMPUTER READABLE FORM: disk
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/988,819
;; FILING DATE: 12-DEC-1997
;; CLASSIFICATION: 536
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/792,019
;; FILING DATE: 03-FEB-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: COOK, ROBERT R.
;; REGISTRATION NUMBER: 31,602
;; REFERENCE/DOCKET NUMBER: A-442A
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 5087 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: 137..138
;; OTHER INFORMATION: /product= "INTERVENING UNSEQUENCED"
;; OTHER INFORMATION: REGION OF >1KB"
US-08-988-819-3

Query Match 65.7%; Score 523.4; DB 3; Length 5087;
Best Local Similarity 99.8%; Pred. No. 6.2e-121;
Matches 524; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 271 ATCTGAACCTACTGGGCCCCCTTTCAACGAGCCAGACTTCAACCCCTCCCGCTGGGG 330
Db |||||
QY 3363 AGCTGAACCTACTGGGCCCCCTTTCAACGAGCCAGACTTCAACCCCTCCCGCTGGGG 3422
Db |||||
QY 331 CAGAGACTCTGCCAGGCCCCCTTTGACTTGGAGGTGTGGCGAAGCCTCAATGACAAAC 390
Db |||||
QY 3423 CAGAGACTCTGCCAGGCCCCCTTTGACTTGGAGGTGTGGCGAAGCCTCAATGACAAAC 3482
Db |||||
QY 391 TGGCGCTGACCCAGAGACTACGAGCCCTACAGCCACCTTCTGTACTTGGTGGCCTCA 450
Db |||||
QY 3483 TGGCGCTGACCCAGAGACTACGAGCCCTACAGCCACCTTCTGTACTTGGTGGCCTCA 3542
Db |||||
QY 451 ACCGTGAGCTGACCCAGAGACTACGAGCCCTACAGCCACCTTCTGTACTTGGTGGCCTCA 510
Db |||||
QY 3543 ACCGTGAGCTGACCCAGAGACTACGAGCCCTACAGCCACCTTCTGTACTTGGTGGCCTCA 3602
Db |||||
QY 511 AGGGCTCTGGGAGAGATTGGGGCGTCAATGGAGCTTGGGCTACCCACTGCCCCAGC 570
Db |||||
QY 3603 AGGGCTCTGGGAGAGATTGGGGCGTCAATGGAGCTTGGGCTACCCACTGCCCCAGC 3662
Db |||||
QY 571 CGCTGCTGGGAGCTGACCCAGAGACTACGAGCCCTACAGCCACCTTCTGTACTTGGTGGCCTCA 630
Db |||||
QY 3663 CGCTGCTGGGAGCTGACCCAGAGACTACGAGCCCTACAGCCACCTTCTGTACTTGGTGGCCTCA 3722
Db |||||
QY 631 AGATGGAGCTTCTGGCTGTGAAGGAGCTGACAGCTTGGCTGTGGCGCTCGGCCAAG 690
Db |||||
QY 691 ACTTCAACCGGCTCAAGAGAGATGAGCCTTCCAGCAGCTGACGTACCCCTGCACTGG 750
Db |||||
QY 3783 ACTTCAACCGGCTCAAGAGAGATGAGCCTTCCAGCAGCTGACGTACCCCTGCACTGG 3842
Db |||||
QY 751 GGGCTCATGGCTTCTGACTTCTGACTTCTGACTTCTGCTTCTGCTCCCC 795
Db |||||
QY 3843 GGGCTCATGGCTTCTGACTTCTGACTTCTGACTTCTGCTTCTGCTCCCC 3887
Db |||||

[illegible]

RESULT 11
US-09-106-182-7
; Sequence 7, Application US/09106182
; Patent No. 6046035
; GENERAL INFORMATION:
; APPLICANT: Shi, Yanggu
; APPLICANT: Ruben, Steve
; TITLE OF INVENTION: Cardiotrophin-Like Cytokine
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc
; STREET: 9410 Key West Ave
; CITY: Rockville
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/106,182
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: US 60/051,053
; FILING DATE: 30-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF385
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 396 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-09-106-182-7

	Query Match	10.1%	Score 80.2;	DB 3;	Length 396;
	Best Local Similarity	96.5%;	Pred. No. 4,7e-11;		
	Matches	82;	Conservative 0;	Mismatches 3;	Indels 0; Gaps 0;
QY	711	AAAGATGAGCCTTCAGCAGCTGCAGTGCACCTGCACCTGGGGGCTCATGGCTTCAGACTT	770		
DB	4	ACGAGGCAGCCTCCAGCAGTGCAGTGCACCTGCACCTGGGGGCTCATGGCTTCAGACTT	63		
QY	771	CTGACCTTCTCCTCTTCGCTCCGCC	795		
DB	64	CTGACCTTCTCCTCTTCGCTCCGCC	88		

```

RESULT 10
US-09-016-534-3
; Sequence 3, Application US/09016534
; Patent No. 6143874
; GENERAL INFORMATION:
; APPLICANT: CHANG, MING-SHI
; APPLICANT: ELLIOTT, GARY S.
; APPLICANT: SARMIENTO, ULLA
; APPLICANT: SENALDI, GIORGIO
; TITLE OF INVENTION: THE NEUROTROPHIC FACTOR NNT-1
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMGEN INC.
; STREET: ONE AMGEN CENTER
; CITY: THOUSAND OAKS
; STATE: CA
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,534
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/792,019
; FILING DATE: 03-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: COOK, ROBERT R.
; REGISTRATION NUMBER: 31,602
; REFERENCE/DOCKET NUMBER: A-442B
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5087 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 137..138
; OTHER INFORMATION: /product= "INTERVENING UNSEQUENCED"
; OTHER INFORMATION: REGION OF >1KB"
US-09-016-534-3

Query Match 65.7%; Score 523.4; DB 3; Length 5087;
Best Local Similarity 99.8%; Pred. No. 6.2e-121;
Matches 524; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 271 ATCTGAACCTACCTGGGGCCCCCTTTCAACAGAGCAGACTTCAACCCCTCCCGGCTGGGG 330
Db 3363 AGCTGAACCTACCTGGGGCCCCCTTTCAACAGAGCCAGACTTCAACCCCTCCCGGCTGGGG 3422

Qy 331 CAGAGACTCTGCCAGGGCCACTGTTGACTTGAGAGGTGTGGCGAAGCCTCAATGACAAAC 390
Db 3423 CAGAGACTCTGCCAGGGCCACTGTTGACTTGAGAGGTGTGGCGAAGCCTCAATGACAAAC 3482

Qy 391 TGGCGCTGACCCAGAACTACAGAGCCCTACAGCCACCTTCTGTGTACTTTCGTGGGCTCA 450
Db 3483 TGGCGCTGACCCAGAACTACAGAGCCCTACAGCCACCTTCTGTGTACTTTCGTGGGCTCA 3542

Qy 451 ACCGTAGGCTGCACGTGCTGAGTGGCGCGCAGCCTGGCCCACTTCTGACACAGCTCC 510
Db 3543 ACCGTAGGCTGCACGTGCTGAGTGGCGCGCAGCCTGGCCCACTTCTGACACAGCTCC 3602

Qy 511 AGGGCCCTGCTGGGAGCAATTGCGGGCGCTCATGGCAGCTCTGGGCTACCCACTGCCCGAGC 570
Db 3603 AGGGCCCTGCTGGGAGCAATTGCGGGCGCTCATGGCAGCTCTGGGCTACCCACTGCCCGAGC 3662

```

RESULT 12

US-09-335-409-1
; Sequence 1, Application US/09335409
; Patent No. 6121029
; GENERAL INFORMATION:
; APPLICANT: Schupp, Thomas
; APPLICANT: Ligon, James
; APPLICANT: Molnar, Istvan
; APPLICANT: Zirkle, Ross
; APPLICANT: Cyr, Devon
; APPLICANT: Goerlach, Joern
; TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
; FILE REFERENCE: 4-30582A
; CURRENT APPLICATION NUMBER: US/09/335,409
; PRIOR FILING DATE: 1999-06-17
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 68750
; TYPE: DNA
; ORGANISM: Sorangium cellulosum
US-09-335-409-1

Query Match 5.6%; Score 44.8; DB 3; Length 68750;
Best Local Similarity 50.0%; Pred. No. 0.12;
Matches 112; Conservative 0; Mismatches 112; Indels 0; Gaps 0;
QY 456 CAGGCTGCCACTGCTGAGCTGCGCGGAGCTGCGCCAGCTTCTGCACAGCTCCAGGGC 515
DB 57992 CAGGTAGCGAGTCGGGAGCCGGGGACGTCGCGCGCCCTTCGGATCCAGCCCGCGC 58051
QY 516 CTGCTGGCAGCAATTGGCGGCGTCATGGCAGCTCTGGGCTACCCACTGCCCGCCGCTG 575
DB 58052 GTGCTGCGCGGATCGGGCGCGTCGAGACCCCGCGGAGTCGAACTCGCGCCCTGCGC 58111
QY 576 CCGTGGGACTGAACTGAGCTGCGGCGTCTGAGCTGCGGCTACCCACTGCCCGCCGCTG 635
DB 58112 GCCCGGCTTCATGCGCGCGTTCGCGGCTATCTATGTCGCTCGCGGATGGG 58171
QY 636 GACGACTTCTGGCTGCTGAAGAGCTGCAGACCTGGCTGTGGCG 679
DB 58172 CTTCAATACGCGCGGCTTCGCGGGGCTCGCCAGCTGTGGCG 58215

RESULT 13

US-09-568-102-1
; Sequence 1, Application US/09568102
; Patent No. 6346404
; GENERAL INFORMATION:
; APPLICANT: Schupp, Thomas
; APPLICANT: Ligon, James
; APPLICANT: Molnar, Istvan
; APPLICANT: Zirkle, Ross
; APPLICANT: Cyr, Devon
; APPLICANT: Goerlach, Joern
; TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
; FILE REFERENCE: 4-30582A
; CURRENT APPLICATION NUMBER: US/09/568,102
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 68750
; TYPE: DNA
; ORGANISM: Sorangium cellulosum
US-09-568-102-1

Query Match 5.6%; Score 44.8; DB 4; Length 68750;
Best Local Similarity 50.0%; Pred. No. 0.12;
Matches 112; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

QY 456 CAGGCTGCCACTGCTGAGCTGCGCGGAGCTGCGCCAGCTTCTGCACAGCTCCAGGGC 515
DB 57992 CAGGTAGCGAGTCGGGAGCCGGGGACGTCGCGCGCCCTTCGGATCCAGCCCGCGC 58051
QY 516 CTGCTGGCAGCAATTGGCGGCGTCATGGCAGCTCTGGGCTACCCACTGCCCGCCGCTG 575
DB 58052 GTGCTGCGCGGATCGGGCGCGTCGAGACCCCGCGGAGTCGAACTCGCGCCCTGCGC 58111
QY 576 CCGTGGGACTGAACTGAGCTGCGGCGTCTGAGCTGCGGCTACCCACTGCCCGCCGCTG 635
DB 58112 GCCCGGCTTCATGCGCGCGTTCGCGGCTATCTATGTCGCTCGCGGATGGG 58171
QY 636 GACGACTTCTGGCTGCTGAAGAGCTGCAGACCTGGCTGTGGCG 679
DB 58172 CTTCAATACGCGCGGCTTCGCGGGGCTCGCCAGCTGTGGCG 58215

RESULT 14

US-09-567-969-1
; Sequence 1, Application US/09567969
; Patent No. 6355457
; GENERAL INFORMATION:
; APPLICANT: Schupp, Thomas
; APPLICANT: Ligon, James
; APPLICANT: Molnar, Istvan
; APPLICANT: Zirkle, Ross
; APPLICANT: Cyr, Devon
; APPLICANT: Goerlach, Joern
; TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
; FILE REFERENCE: 4-30582A
; CURRENT APPLICATION NUMBER: US/09/567,969
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 68750
; TYPE: DNA
; ORGANISM: Sorangium cellulosum
US-09-567-969-1

Query Match 5.6%; Score 44.8; DB 4; Length 68750;
Best Local Similarity 50.0%; Pred. No. 0.12;
Matches 112; Conservative 0; Mismatches 112; Indels 0; Gaps 0;
QY 456 CAGGCTGCCACTGCTGAGCTGCGCGGAGCTGCGCCAGCTTCTGCACAGCTCCAGGGC 515
DB 57992 CAGGTAGCGAGTCGGGAGCCGGGGAACTGCGCGCCCTTCGGATCCAGCCCGCGC 58051
QY 516 CTGCTGGCAGCAATTGGCGGCGTCTGAGCTCTGGGCTACCCACTGCCCGCCGCTG 575
DB 58052 GTGCTGCGCGGATCGGGCGCGTCGAGACCCCGCGGAGTCGAACTCGCGCCCTGCGC 58111
QY 576 CCGTGGGACTGAACTGAGCTGCGGCGTCTGAGCTGCGGCTACCCACTGCCCGCCGCTG 635
DB 58112 GCCCGGCTTCATGCGCGCGTTCGCGGCTATCTATGTCGCTCGCGGATGGG 58171
QY 636 GACGACTTCTGGCTGCTGAAGAGCTGCAGACCTGGCTGTGGCG 679
DB 58172 CTTCAATACGCGCGGCTTCGCGGGGCTCGCCAGCTGTGGCG 58215

RESULT 15

US-09-568-480-1
; Sequence 1, Application US/09568480
; Patent No. 6355458
; GENERAL INFORMATION:
; APPLICANT: Schupp, Thomas
; APPLICANT: Ligon, James
; APPLICANT: Molnar, Istvan
; APPLICANT: Zirkle, Ross


```
; APPLICANT: Cyr, Devon
; APPLICANT: Goerlach, Joern
; TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
; FILE REFERENCE: 4-30582A
; CURRENT APPLICATION NUMBER: US/09/568,480
; CURRENT FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: 09/335,409
; PRIOR FILING DATE: 1999-06-17
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 68750
; TYPE: DNA
; ORGANISM: Sorangium cellulosum
US-09-568-480-1

Query Match      5.6%; Score 44.8; DB 4; Length 68750;
Best Local Similarity 50.0%; Pred. No. 0.12; Indels 0; Gaps 0;
Matches 112; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

QY      456 CAGGCTGCCACTGTGAGCTGCGCGGAGCGGGGAACTGCGGCGGCCCTTCGGGATCCACGCCCGCGGC 515
Db      57992 CAGGTAGCGAGTTCGGGAGCGCGGGGAACTGCGGCGGCCCTTCGGGATCCACGCCCGCGGC 58051

QY      516 CTGCTGGGACAGTTCGGGCGTCATGGCAGCTCTGGGCTACCCACTGCCCGCGCGCTG 575
Db      58052 GTGCTGCCCGCGATCGGGCGCTGAGACCCCGCGGAGTCGAACTCGCGCCCTGCGC 58111

QY      576 CCTGGGACTGAACCCACTTGGACTTCCTGGCCCTGCCCGACAGTTCCTTCCAGAGATG 635
Db      58112 GCCCGGCTTCATGCCGCGTCCCGCTGCGGCTATCTATGTCGCTCGCGGAGATGGG 58171

QY      636 GACGACTTCTGGCTCTGAAGAGCTGCAGACTGGCTGTGGG 679
Db      58172 CTTCAATACGGCCCGCGCTTCGGGGGCTCGCCGAGCTGTGGG 58215
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Search completed: August 16, 2004, 09:35:11
Job time : 62.7376 secs

Result No.	Score	Query Match	Length	DB	ID	Description
1	124.5	10.2	203	2	JC4645	cardiotrophin-1 -
2	118.5	9.7	203	2	I49153	cardiotrophin-1 -
3	92	7.5	332	2	G86182	hypothetical prote
4	91.5	7.5	201	2	G03212	cardiotrophin-1 -
5	91.5	7.5	182	2	I48378	hairless protein -
6	91	7.4	195	2	JH0680	ciliary neurotroph
7	89.5	7.3	1313	2	T38943	probable guanine n
8	89	7.3	733	2	D83588	conserved hypothet
9	87	7.1	955	2	T00247	zinc finger protei
10	87	7.1	1561	2	T00248	zinc finger protei
11	86.5	7.1	840	2	T34916	transferase - Stre
12	85.5	7.0	560	2	C38604	poly(3-hydroxyalka
13	84.5	6.9	389	2	F72511	probable cystathio
14	84	6.9	200	2	F32633	hypothetical prote
15	84	6.9	411	2	F75439	probable cell wall
16	84	6.9	559	2	F71327	probable apolipop
17	83	6.8	452	2	A35602	tallness, (tll) pro
18	82.5	6.7	542	2	A82965	hypothetical prote
19	82.5	6.7	723	2	E38749	3-phosphatidylino
20	82	6.7	179	2	T04584	TMV resistance pro
21	81	6.6	479	2	AG2726	DNA photolyase (m
22	81	6.6	479	2	C92708	blue-light photore
23	80.5	6.6	353	2	AB1823	hypothetical prote
24	80.5	6.6	512	2	S21171	activin receptor S
25	80	6.5	200	1	UNR7C7	ciliary neurotroph
26	80	6.5	460	2	D75493	cell division cycl
27	80	6.5	2261	1	A42548	genome polypeptid
28	79	6.4	812	2	T34180	hypothetical prote
29	79	6.4	1220	2	AD0125	exodeoxyribonucle

N;Alternate names: growth-promoting activity protein
 C;Species: Gallus gallus (Chicken)
 C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jul-2000
 C;Accession: JH0680; PQ0057
 R;Leung, D.W.; Parent, A.S.; Cachianes, G.; Esch, F.; Coulombe, J.N.; Nikolic, K.; Ecker
 Neuron 8, 1045-1053, 1992
 A;Title: Cloning, expression during development, and evidence for release of a trophic f
 A;Reference number: JH0680; MUID:92304573; PMID:1610564
 A;Accession: JH0680
 A;Molecule type: mRNA
 A;Residues: 1-195 <LEU>
 A;Cross-references: GB:M80827; NID:g211822; PIDN:AAA48784.1; PID:g211823
 A;Experimental source: eye
 R;Eckstein, F.P.; Esch, F.; Holbert, T.; Blacher, R.W.; Nishi, R.
 Neuron 4, 623-631, 1990
 A;Title: Purification and characterization of a trophic factor for embryonic peripheral
 A;Reference number: PQ0057; MUID:90211978; PMID:2322465
 A;Accession: PQ0057
 A;Molecule type: protein
 A;Residues: 155-166, 'X', 168-175 <ECK>
 A;Experimental source: sciatic nerves
 C;Comment: This is a neurotrophic protein.
 C;Superfamily: ciliary neurotrophic factor
 C;Keywords: growth factor

Query Match 7.4%; Score 91; DB 2; Length 195;
 Best Local Similarity 27.3%; Pred. No. 0.53;
 Matches 51; Conservative 21; Mismatches 83; Indels 32; Gaps 9;

QY 46 LTVLEHQLRLSLAGTYLNYLPGPPNEPDPNPRGLGAETLPATVDLEWRSNDKRLTQ 105
 Db 23 LARKRSVDTLLDIYVERQ-----LDASISVAADGVPTAAV--ERWAEQTGTORLLD 75

QY 106 N---YEAYSHLLCYLRGLNRQA---ATAELRSLA-----HPTCTSLQGLGSIAGVMA 152
 Db 76 NLAAVRAFETLLAQMLEBQRELLGDTDAELGPALANMLQVSFVYHLELL-----ELE 130

QY 153 ALGYPLOPLPGTETPTPGPAH--SDFLQKMDDFWLKELQTNWRSKDFNRLKKMQP 211
 Db 131 SRGAPAE--GSPF---PAPRLSLFEQKLRGLRVLRLAQNAVRSVRDLRQLSKHGP 184

QY 212 PAAAVTL 218
 Db 185 SGAALGL 191

RESULT 7
 T38943
 probable guanine nucleotide binding protein - fission yeast (Schizosaccharomyces pombe)
 C;Species: Schizosaccharomyces pombe
 C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
 C;Accession: T38943
 R;Skellton, J.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
 submitted to the EMBL Data Library, May 1997
 A;Reference number: Z21819
 A;Accession: T38943
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-1313 <SKE>
 A;Cross-references: EMBL:Z95396; PIDN:CA808769.1; GSPDB:GN00066; SPDB:SPAC57A7.11
 A;Experimental source: strain 972h-; cosmid c57A7
 C;Genetics:
 A;Gene: SPDB:SPAC57A7.11
 A;Map position: 1

Query Match 7.3%; Score 89.5; DB 2; Length 1313;
 Best Local Similarity 22.8%; Pred. No. 8;
 Matches 61; Conservative 32; Mismatches 69; Indels 105; Gaps 14;

QY 15 LCTVWLHLPAV--PALNR-----TGDPGGPGSI-----QKYDITRYLEHQLRS 56
 Db 811 LAFQLHLPAHLKASLSDTNSVTSDPKHPFVPSVSENKILNRSFSLTRSLKGLALS 870

QY 57 LAG-----TYINYL-----GPP-FNEPDPNPRGLGAETLPATVDL 91
 Db 871 LAGSDRAESELLNGENKPAESNLHLTSAKVGPFPFAFNELEY-----QSELD 919

QY 92 EVKRSND-----KRLTONYEAYSHLLCYLRGL---NEQATAELRLRSIAHCTS 139
 Db 920 PLTSYLFDSRKYFTPEQWRPNDEDDPGS--ICYNORLWRNNEKLIIVTRPLAESTYN 977

QY 140 -----LQGLLSIAGVMAALGYPLPQPLFGTEPTWPGPAHSDFLQKMDDFWLKE--- 190
 Db 978 GRWNQQLMFPNTIA-----PRKLMFHQFEDQLITLGDKI 1013

QY 191 LQWLWRSKDFNRLKKMQPPAAAVT 217
 Db 1014 IQVWDWR-----NRLNSFKTSASAT 1036

RESULT 8
 D83588
 conserved hypothetical protein PA0454 [imported] - Pseudomonas aeruginosa (strain PA01)
 C;Species: Pseudomonas aeruginosa
 C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
 C;Accession: D83588
 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lam,
 .; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
 A;Reference number: A82950; MUID:20437337; PMID:10984043
 A;Accession: D83588
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-733 <STO>
 A;Cross-references: GB:AE004483; GB:AE004091; NID:g9946313; PIDN:LAG03843.1; GSPDB:GN001
 A;Experimental source: strain PA01
 C;Genetics:
 A;Gene: PA0454
 C;Superfamily: hypothetical protein Hii680

Query Match 7.3%; Score 89; DB 2; Length 733;
 Best Local Similarity 26.6%; Pred. No. 4.3;
 Matches 58; Conservative 26; Mismatches 66; Indels 68; Gaps 13;

QY 28 LARTGPGGPGSIQKTYDLTRYLE-----HQLRSLAGTYLNYLPGPPNPD--FNPP 77
 Db 230 LNRLGHRGPGKV-----SRYKLVFYIAQDVHERASSSHYPYNLAEAFESDVLFRQ 283

QY 78 RL-----GAETLPATVDLEWRSNDKRLTONYEAYSHLLCYLRGLNRQAATAELRR 131
 Db 284 RLINQOGKACQALRA-----IRLQPFDFYA-----DRELALEDLQA 320

QY 132 SLAHF-----CTSLQGLLSIAGVMAALGYPLPQPLFGTEPTWPGPAHSDFLQKMDDFWL 187
 Db 321 SLEHLRQOSNPANKGLRSL-GALANLTLTLDRKLAGA-----SNPDAIADQDSAL 371

QY 188 LKELQTLWRSKDFNRLKKMQPPAAAVTLHLGAHG 224
 Db 372 LDRSP-----RSLKDAFERLRQOLTP-----TSLLPRHG 400

RESULT 9
 T00247
 zinc finger protein wiz - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 05-Nov-1999
 C;Accession: T00247
 R;Matsumoto, K.; Ishii, N.; Yoshida, S.; Shiosaka, S.; Wanaka, A.; Tohyama, M.
 submitted to the EMBL Data Library, March 1998
 A;Description: Molecular cloning and distinct developmental expression pattern of splice
 A;Reference number: Z14130
 A;Accession: T00247
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA

A;Residues: 1-955 <MAT>
A;Cross-references: EMBL:AB012266; NID:d1227741; PIDN:BAA32791.1; PID:d1033757
A;Experimental source: brain
C;Genetics: wiz
A;Gene: wiz

Query Match 7.1%; Score 87; DB 2; Length 955;
Best Local Similarity 27.8%; Pred. No. 9.2; Indels 24; Gaps 7;
Matches 35; Conservative 19; Mismatches 48; Indels 24; Gaps 7;
QY 22 LPAPALNRTGDPGPGPSIQKTYDLYLRYLHQLRSLAG---TYLNYLGP-----PFNEPD 73
Db 615 LPLSPLASRKGKPGAGPT-----QVPR--ELSLSPITGSKPSAASYLGPVATKRPLOEDR 667
QY 74 FNPPLGAEITLPRATVDLEWRSINDKRLTQNYEAYSHLLCYLRLGL---NRQATAELR 130
Db 668 FLPAEVKAKTYIQTELPFKA-KTLHEK-----TSHSSTEACCELCGLYFENRKALASHAR 721
QY 131 RSLAHF 136
Db 722 AHLRQF 727

RESULT 10
T00248
zinc finger protein wizL - mouse
C;Species: Mus musculus (house mouse)
C;Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 05-Nov-1999
R;Matsumoto, K.; Ishii, N.; Yoshida, S.; Shiozaka, S.; Wanaka, A.; Tohyama, M.
submitted to the EMBL Data Library, March 1998
A;Description: Molecular cloning and distinct developmental expression pattern of splice
A;Reference number: Z14130
A;Accession: T00248
A;Status: preliminary; translated from GB/EMBL/DDSDJ
A;Molecule type: mRNA
A;Residues: 1-1561 <MAT>
A;Cross-references: EMBL:AB012265; NID:d1227740; PIDN:BAA32790.1; PID:d1033756
A;Experimental source: brain
C;Genetics: wiz
A;Gene: wiz

Query Match 7.1%; Score 87; DB 2; Length 1561;
Best Local Similarity 27.8%; Pred. No. 17; Indels 24; Gaps 7;
Matches 35; Conservative 19; Mismatches 48; Indels 24; Gaps 7;
QY 22 LPAPALNRTGDPGPGPSIQKTYDLYLRYLHQLRSLAG---TYLNYLGP-----PFNEPD 73
Db 1221 LPLSPLASRKGKPGAGPT-----QVPR--ELSLSPITGSKPSAASYLGPVATKRPLOEDR 1273
QY 74 FNPPLGAEITLPRATVDLEWRSINDKRLTQNYEAYSHLLCYLRLGL---NRQATAELR 130
Db 1274 FLPAEVKAKTYIQTELPFKA-KTLHEK-----TSHSSTEACCELCGLYFENRKALASHAR 1327
QY 131 RSLAHF 136
Db 1328 AHLRQF 1333

RESULT 11
T34916
transferase - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 02-Sep-2000
R;Oliver, K.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, January 1998
A;Reference number: Z21558
A;Accession: T34916
A;Status: preliminary; translated from GB/EMBL/DDSDJ
A;Molecule type: DNA
A;Residues: 1-640 <OLI>
A;Cross-references: EMBL:AL021409; PIDN:CAA16181.1; GSPDB:GNC00070; SCODEB:SC3F7.10

A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCODEB:SC3F7.10
C;Superfamily: glycine C-acetyltransferase homology
F;287-624/Domain: glycine C-acetyltransferase homology <GCA>

Query Match 7.1%; Score 86.5; DB 2; Length 640;
Best Local Similarity 27.2%; Pred. No. 6.1; Indels 57; Gaps 9;
Matches 50; Conservative 13; Mismatches 64; Indels 57; Gaps 9;
QY 22 LPAPALNRTGDPGPGPSIQKTYDLYLRYLHQLRSLAGTYLNYLGPFPNEPD 78
Db 100 LPAPVA-EGTGDVTVAVVAAAMRQYQYORHQLGDLADLEG-----E 140
QY 79 LGAEITLPRATVDLEWRSINDKRLTQNYEAYSHLLCYLRLGLNROQATAELRSLAHFCT 138
Db 141 LGVDSVVLTSSVAEA---TERLGLT-----GAAPDAAGATTTLALA---D 179
QY 139 SLOGLLGSTAGYMAALGYPLQPLPGTEPTWTPGPAHSDFLQKDDFWLLKELQTLWRS 198
Db 180 ALRGL-----VAAAPGTAVPEAAPATGAA-APAPGRSGNAP-----APGADGHDHS 225
QY 199 AKDF 202
Db 226 MKDF 229

RESULT 12
C38604
poly(3-hydroxyalkanoate) polymerase (EC 2.7.7.-) 3 - Pseudomonas oleovorans
C;Species: Pseudomonas oleovorans
C;Date: 23-Aug-1991 #sequence_revision 23-Aug-1991 #text_change 08-Sep-2000
C;Accession: C38604
R;Huisman, G.W.; Woonink, E.; Meima, R.; Kazemier, B.; Terpstra, P.; Witholt, B.
J. Biol. Chem. 266, 2191-2198, 1991
A;Title: Metabolism of poly(3-hydroxyalkanoates) (PHAs) by Pseudomonas oleovorans. Ident
A;Reference number: A38604; MUID:91115830; PMID:1989978
A;Accession: C38604
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-560 <HUI>
A;Cross-references: GB:M58445; NID:g151441; PIDN:AAA25934.1; PID:g151444
C;Superfamily: poly(3-hydroxyalkanoic acid) synthase phbc
C;Keywords: nucleotidyltransferase

Query Match 7.0%; Score 85.5; DB 2; Length 560;
Best Local Similarity 30.2%; Pred. No. 6.4; Indels 29; Gaps 7;
Matches 38; Conservative 17; Mismatches 42; Indels 29; Gaps 7;
QY 77 PRLGAEITLPRATVDLEWRSINDKRLTQNYEAYSHLLCYLRLGLNROQATAELRSL--A 134
Db 5 PAKGTPPLPATSMNVQ-----NAILGLRGR-----DLISLRNVSRQS-----LEHPLHTA 50
QY 135 HFCTISLQGLLSIAGVMAALGYPLQPLPG-----TEPTWTPGPAHSDFLQKDDFWLLKE 190
Db 51 HLLALGQLGRV-----ILGDTPLQNPDRPFRSDFTWSONPYRGLQA-----YLAWQ 101
QY 191 LQTLW 196
Db 102 KQTRLW 107

RESULT 13
F72511
probable cystathionine gamma-synthase APE2068 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C;Accession: F72511
R;Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A;Reference number: A72450; MUID:99310339; PMID:10382966

A:Accession: F72511
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-389 <KAW>
A:Cross-references: DDBJ:AP000063; NID:g5105654; PIDN:BAA81078.1; PID:g5105766
A:Experimental source: strain K1
C:Genetics:
A:Gene: APE2068
C:Superfamily: O-succinylhomoserine (thiol)-lyase

Query Match
Best Local Similarity 22.9%; Score 84.5; DB 2; Length 389;
Matches 47; Conservative 19; Mismatches 78; Indels 61; Gaps 8;

QY 43 TYDLTRYLEHQRLSAGYVNLVNGPPFNEPDPRLGAETLPRATVDELYVWRSI----- 97
Db 107 TYGSTRSLEMLSSITGIEVRLAGPPWED-----LLDLVCWADLIIVES 150
QY 98 --NDKRLRTQNYEAYSHLLCYLRGNROATAELR-----RSL--AHFCTS 139
Db 151 MANPTLRVPP-----LSGIYREAGSGVGVVDNFTPIAYRPLRGAYH--S 197
QY 140 LQGLGSIAGVMAALGYPLPQPL-EGTEPTWTTPGPAHSDFLQKMDDFWLLKELQTLWRS 198
Db 198 LESLTKYIAGHNDVVGSGLSGRVEDLEPLNMKILCTIQPIDAY-----LAWRG 249
QY 199 AKDFNRLKKQWPPAAAVTLHLGAH 223
Db 250 MKTLKARFEAQSRAAWEVAEWLESH 274

RESULT 14
AD3633
hypothetical protein BMEI10989 [imported] - Brucella melitensis (strain 16X)
C:Species: Brucella melitensis
C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C:Accession: AD3633
R:DeiVecchio, V.G.; Kapatal, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Jeteles
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
A:Reference number: AD3252; PMID:11756688
A:Accession: AD3633
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-200 <KUR>
A:Cross-references: GB:AE008918; PIDN:AAL54231.1; PID:g17985203; GSPDB:GN00191
A:Experimental source: strain 16X
C:Genetics:
A:Gene: BMEI10989
A:Map position: 11

Query Match
Best Local Similarity 24.3%; Score 84; DB 2; Length 200;
Matches 56; Conservative 22; Mismatches 84; Indels 68; Gaps 13;

QY 10 GMLACLCTVLMHLPAPVPAALNRTGDPGPGSIQKTYDILTRYLEHQRLSAGYVNLVNGPPF 69
Db 2 GLLAGAAV---LPSLPAAKTAQQAAMPNATSPHQADVYL---LRGFADIFSTGI---- 51
QY 70 NEPDFNPRLGAETLPRATVDEY-----WESLNDKRLTQNYEAYSHLLCYLRG--LNR 122
Db 52 -----DEIGAE-LQAAGVNAHVCGHAARVNLN--RIVADQOQNGHLPVVLIGHSLGA 101
QY 123 QAA---TAEFLRRSLAHFCTSISQGLLSTAGVMAALGYPLPQPLPGT-----EPTW 169
Db 102 NAAIYIAEELER-----RGIAVDYMATPATG---PDPLPCNVRRVNVFFQKHGW 149
QY 170 ----TPGPAHSDFLQKMDDFWLLKELQTLWRSADFNRLKKKQWPPAAA 215
Db 150 GLPLVPGPRFHGHLEND-----FSNAKDVGHFNIEKQRPLOA 187

RESULT 15

F75439
probable cell wall synthesis protein - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C:Accession: F75439
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; PMID:20036896; PMID:10567266
A:Accession: F75439
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-411 <WHI>
A:Cross-references: GB:AE001958; GB:AE005513; NID:g6458805; PIDN:AAF10649.1; PID:g645880
A:Experimental source: strain R1
C:Genetics:
A:Gene: DRI076
A:Map position: 1

Query Match
Best Local Similarity 24.8%; Score 84; DB 2; Length 411;
Matches 56; Conservative 25; Mismatches 77; Indels 70; Gaps 11;

QY 2 DLRAGDSWGMCLACTVLMHLPAPVPAALNRTGDPGPGSIQKTYDILTRYLEHQRLSAGTY 61
Db 212 EVLAADRWRALRAELFSEMSLRPGVPIILLSGG-GRGHYAAADVLT-----ELGNL-GRA 264
QY 62 LNYLGPPFNEPDPRLGAETLPRATVDELYVWRSLNDKRLTQNYEAYSHLLCYLRGLN 121
Db 265 VQVLVPASRQGE-----GTETIGGATV-----HHLGFRDLPL 296
QY 122 ROATAELRRSLAHFCTSISQGLLSTAGV---MAALGYPLP--QPLPGTEPTWTTPGAH 175
Db 297 RLIAASDL-----VVGKAGGLTVAEATLGVPLVIYADIPQGE-----EHN 337
QY 176 SDFLQKMDDFWLLKELQTLWV-NSAKDFNRLKKKQWPPAAAVTLHLGA 222
Db 338 ADPLERHG-----AGLWARARHDVRLVLRALDPAEHARLSAGA 376

Search completed: August 10, 2004, 06:44:11

Job time : 16.5 secs

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OM protein - protein search, using sw model

Run on: August 10, 2004, 06:43:28 ; Search time 8 Seconds
(without alignments)
1464.473 Million cell updates/sec

Title: US-09-931-704-2

Perfect score: 1226

Sequence: 1 MDLRAGDSWGMCLCTVLW.....KKKMQPPAAAATLHLGAGHF 225

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	218.5	17.8	204	1	CTF2 MOUSE
2	124.5	10.2	203	1	CTF1 RAT
3	118.5	9.7	203	1	CTF1 MOUSE
4	96.5	7.9	455	1	CTF2 MOUSE
5	94	7.7	423	1	CST MOUSE
6	93	7.6	619	1	NXF1 HUMAN
7	91.5	7.5	201	1	CTF1 HUMAN
8	91.5	7.5	1182	1	HAIR MOUSE
9	91	7.4	195	1	CNTF CHICK
10	89.5	7.3	1313	1	MIPL SCHPO
11	87.5	7.1	1181	1	HAIR RAT
12	86	7.0	1009	1	MZB2 HUMAN
13	85.5	7.0	560	1	PHAC PSBOL
14	84	6.9	200	1	CNTF PIG
15	83	6.8	452	1	TILL DROME
16	82.5	6.7	1189	1	HAIR HUMAN
17	82	6.7	724	1	P5B5 BOVIN
18	81	6.6	291	1	YM32 MYCTU
19	81	6.6	618	1	NXF1 RAT
20	80.5	6.6	294	1	HUPK RHOCA
21	80.5	6.6	870	1	BCA1 HUMAN
22	80.5	6.6	1473	1	NAL1 HUMAN
23	80	6.5	200	1	CNTF RAT
24	80	6.5	422	1	V140 HUMAN
25	80	6.5	2261	1	RRPL MUMPM
26	79	6.4	552	1	MFP2 MOUSE
27	79	6.4	1621	1	ALK MOUSE
28	78.5	6.4	390	1	YL28 STRCO
29	78.5	6.4	1102	1	CARS STRCO
30	78	6.4	3680	1	DMD CANFA
31	77	6.3	585	1	UL84 HCMVA
32	77	6.3	587	1	UL84 HCMVT
33	76.5	6.2	571	1	ATKA MYCTU

34	76.5	6.2	572	1	SYM AERPE
35	76.5	6.2	995	1	MZB2 PIG
36	76	6.2	296	1	RECO ANASP
37	76	6.2	416	1	IGAS STRCJ
38	76	6.2	1001	1	PTPX MOUSE
39	76	6.2	1132	1	BAT3 HUMAN
40	75.5	6.2	830	1	VPB3 HUMAN
41	75	6.1	199	1	CNTF RABIT
42	75	6.1	315	1	YNF1 ECOLI
43	75	6.1	343	1	DFRA SYN3
44	75	6.1	450	1	TLL DROVI
45	75	6.1	917	1	SYI STAAH

ALIGNMENTS

RESULT 1
CTF2 MOUSE
ID CT2_MOUSE STANDARD; PRT; 204 AA.
AC P3714;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Cardiotoxin-2 precursor (CT-2).
GN CTF2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Hasegawa M., Habu K., Adachi Y., Natori O.;
RT "Cardiotoxin-2 increases the platelet counts with splenomegaly in vivo".
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Increases the platelet count associated with splenomegaly.
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -!- SIMILARITY: Belongs to the IL-6 superfamily.
CC -----
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CC -----
DR EMBL; AB125661; BAD01485.1; --
KW Cytokine; Signal.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 204 CARDIOTOXIN-2.
FT CARBOHYD 44 44 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 204 AA; 22000 MW; B05566C1E7C3D9C0 CRC64;
Query Match 17.8%; Score 218.5; DB 1; Length 204;
Best Local Similarity 30.3%; Pred. No. 2.8e-13;
Matches 64; Conservative 31; Mismatches 81; Indels 35; Gaps 6;
QY 14 CLCTVWHLPAVALNRTGDPGPGPSIOKTYDLYLEHQLRSLAGTYLVNLPFNPDP 73
Db 10 CLLSLL-----LPPLSPAAPISPEPIQAVSLALYMQKNTSALLQTVLHQGSPSPDG 64
QY 74 FNPPRLGAEITPRATVLEWRSNDKRLRLTQNTVYAYSHLLCYLR-----G 119
Db 65 FSAPELQLSLTPSAVSPKTHAMEDAERLGRAQAFALATQHLQVGDQSYLNPSPFI 124
QY 120 LNRQATAEELRSLAHFCTSLQGLGSGTAGVAAAGYPLPQPLPCTET--WTPGPAHSD 177
Db 125 LIAQGAARLR-----AQGLGNMAAINTALGLPFP-----EDTLGFVPFGA-SA 170
QY 178 FLQRMDFWLLKELQTLWRSKADFNRLKKK 208

```
DB 171 PERKCRGIVTREYGHWTDRVRLALLKAK 201
RESULT 2
CTF1_RAT
ID_CTF1_RAT STANDARD; PRT; 203 AA.
AC Q63086;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Cardiotrophin-1 (CT-1).
GN CTF1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Heart;
RX MEDLINE=96193659; PubMed=8604995;
RA Ishikawa M., Saito Y., Miyamoto Y., Kuwahara K., Ogawa E.,
RA Nakagawa O., Harada M., Masuda I., Nakao K.;
RT "cDNA cloning of rat cardiotrophin-1 (CT-1): augmented expression of
CT-1 gene in ventricle of genetically hypertensive rats.";
RL Biochem. Biophys. Res. Commun. 219:377-381(1996).
CC -!- FUNCTION: Induces cardiac myocyte hypertrophy in vitro. Binds to
CC and activates the ILST/gp130 receptor.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed in the ventricle and atrium of adult
CC rats. Also detected in the lung, kidney, liver, skeletal muscle,
CC stomach and urinary bladder. Not detected in brain, colon, testis,
CC spleen or thymus. Overexpressed in the ventricles in the case of
CC hypertension and hypertrophy.
CC -!- SIMILARITY: Belongs to the IL-6 superfamily.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC
CC EMBL; D78591; BAA1427.1; -.
CC PIR; JC4645; JC4645.
CC Cytokine.
CC KW Cytokine.
CC SEQUENCE 203 AA; 21439 MW; DF8B921A2FA1C832 CRC64;
Query Match 10.2%; Score 124.5; DB 1; Length 203;
Best Local Similarity 28.1%; Pred. No. 0.00018;
Matches 50; Conservative 24; Mismatches 85; Indels 19; Gaps 5;
QY 40 IQKTYDITRYLEHQLRSLACTYLYLGGPPNPPRL---GATLPRATVDLEWRS 96
DB 27 IROTHNLARLLTKYAQLLEEVYQQQGEPLGPGFPPLPLAGLGGPAPSHAGLPV--- 83
QY 97 LNDKRLTONYEAYSHLLCYLRLGNLQAA-----TAEIRESLAHFCTSLQGLLGSTAGVM 151
DB 84 ---SERLRQDAALSAIPALLDVRRRQAEINPAPRLRLSLRLEDAARQVRLGAATVTL 140
QY 152 AALGYPL---PLPPLGTEPTTPGPAHSDFLOKDDDFLLKEQLTWLWRSKDFNRL 205
DB 141 AALGAARGCPPEPVVATLFTANSTAGIFSAKVLGHVGVGLYGEWVSRTEGLQL 197
RESULT 3
ID_CTF1_MOUSE STANDARD; PRT; 203 AA.
AC Q60753;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Cardiotrophin-1 (CT-1).
GN CTF1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryonic stem cells;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
QY 40 IQKTYDITRYLEHQLRSLACTYLYLGGPPNPPRL---GATLPRATVDLEWRS 96
DB 27 IROTHNLARLLTKYAQLLEEVYQQQGEPLGPGFPPLPLAGLGGPAPSHAGLPV--- 83
QY 97 LNDKRLTONYEAYSHLLCYLRLGNLQAA-----TAEIRESLAHFCTSLQGLLGSTAGVM 151
DB 84 ---SERLRQDAALSAIPALLDVRRRQAEINPAPRLRLSLRLEDAARQVRLGAATVTL 140
QY 152 AALGYPL---PLPPLGTEPTTPGPAHSDFLOKDDDFLLKEQLTWLWRSKDFNRL 205
DB 141 AALGAARGCPPEPVVATLFTANSTAGIFSAKVLGHVGVGLYGEWVSRTEGLQL 197
```

Qy	105	QNYEAYSHLLCYRLGRLNQATAEALRSLAHFCTSIQLGLSGTAGVWAALGYPLPOP----	167
Dd	117	-----VDPHFL-LLPHTTWTFPTAEVLISAFHCKFKLGGKYQL-----PLEQPVR	162
Qy	162	-----LPQTETPTWTPGAH-----SDFLKMDDEFLLKELQTLW----WRSAKDF	202
Dd	163	LLLSLSLQSTMCSATAGNLRKLTYTLNNCIFSSRLPELHSHWLND-RINLAHWRSRAQS	221
Qy	203	NELKKMQPPAAAVTLHLGAHCF 225	
Dd	222	SRYFSQLEIMAHILSQFFGTTFP 244	
RESULT 5			
CST_MOUSE			
ID	CST_MOUSE	STANDARD;	PRT; 423 AA.
AC	Q9DHE4; Q9D8V6;		
DT	28-FEB-2003 (Rel. 41, Created)		
DE	28-FEB-2003 (Rel. 41, last sequence update)		
DE	10-OCT-2003 (Rel. 42, last annotation update)		
DE	Galactosylceramide sulfotransferase (EC 2.8.2.11) (GalCer		
DE	sulfotransferase) (Cerbroside sulfotransferase) (3'-		
DE	phosphoadenylylsulfate:galactosylceramide 3'-sulfotransferase)		
DE	(3'-Phosphoadenosine-5-phosphosulfate:GalCer sulfotransferase).		
CS	OR GCST.		
GN	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.		
ON	NCBI_TaxID=10090;		
RX	[1]_		
RP	SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.		
RC	TISSUE=Kidney;		
RX	MEDLINE=20193614; PubMed=10727929;		
RA	Hirahara Y., Tsuda M., Wada Y., Honke K.;		
RT	"cDNA cloning, genomic cloning, and tissue-specific regulation of		
RT	mouse cerebroside sulfotransferase.";		
RT	Eur. J. Biochem. 267:1909-1917(2000).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=C57BL/6J; TISSUE=Pancreas;		
RX	MEDLINE=21085660; PubMed=11217851;		
RA	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,		
RA	Aizawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,		
RA	Arakawa K., Izawa M., Nishi K., Kiyesawa H., Kondo S., Yamataka I.,		
RA	Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,		
RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,		
RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochiya H.,		
RA	Kuehl P., Lewis S., Matsuo Y., Nikolaio D., Pesole G., Quackenbush J.,		
RA	Schimi L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,		
RA	Sakai K., Okido T., Furuno M., Anon H., Baldarelli R., Barsh G.,		
RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,		
RA	Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,		
RA	Gustinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,		
RA	Lyonis P., Marchionni L., Mashima J., Mazzarelli J., Morbaerts P.,		
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,		
RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,		
RA	Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,		
RA	Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,		
RA	Hayashizaki Y.;		
RT	"Functional annotation of a full-length mouse cDNA collection.";		
RT	Nature 409:685-690(2001).		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Colon;		
RX	MEDLINE=22388257; PubMed=12477932;		
RA	Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,		
RA	Altkausner R.D., Collins F.S., Wegner L., Shenmen C.N., Schuler G.D.,		
RA	Hopkins R.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,		
RA	Diatchenko L., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,		
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,		
RA	Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,		
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prace C.		

SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RA Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K.,
 RA Nakajima Y., Mizuno T., Morinaga M., Tanigami A., Fujiwara T., Ono T.,
 RA Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y., Ota T., Suzuki Y.,
 RA Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y.,
 RA Isogai T., Sugano S.;
 RT "NEDO human cDNA sequencing project.";
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 RN (5)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain, and Placenta;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Brownstein M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN (6)
 RP SEQUENCE OF 61-619 FROM N.A.
 RC TISSUE=Lymphocytes;
 RA MEDLINE=97318898; PubMed=9175835;
 RA Yoon D.-W., Lee H., Seol W., DeMaria M., Rosenzweig M., Jung J.U.;
 RT "Rap: a novel cellular protein that interacts with tip of herpesvirus
 RT saimiri and induces lymphocyte aggregation.";
 RL Immunity 6:571-582(1997).
 RN (7)
 RP FUNCTION
 RA MEDLINE=98325379; PubMed=9660949;
 RA Grueter P., Taberner C., von Kobbe C., Schmitt C., Saavedra C.,
 RA Bachi A., Wilm M., Feilber B.K., Izaurralde E.;
 RT "RAP, the human homolog of Mex67p, mediates CTE-dependent RNA export
 RT from the nucleus.";
 RL Mol. Cell 1:649-659(1998).
 RN (8)
 RP CHARACTERIZATION.
 RA MEDLINE=21282872; PubMed=11259411;
 RA Braun I.C., Herold A., Rode M., Conti E., Izaurralde E.;
 RT "Overexpression of TAP/p15 heterodimers bypasses nuclear retention and
 RT stimulates nuclear mRNA export.";
 RL J. Biol. Chem. 276:20536-20543(2001).
 RN (9)
 RP CHARACTERIZATION.
 RA MEDLINE=20132240; PubMed=10668806;
 RA Bachi A., Braun I.C., Rodriguez J.P., Pante N., Ribbeck K.,
 RA von Kobbe C., Kutay U., Wilm M., Gorlich D., Carmo-Fonseca M.,
 RA Izaurralde E.;
 RT "The C-terminal domain of TAP interacts with the nuclear pore complex
 RT and promotes export of specific CTE-bearing RNA substrates.";
 RL RNA 6:136-156(2000).
 RN (10)
 RP MUTAGENESIS.
 RA MEDLINE=21151125; PubMed=11256625;
 RA Suyama M., Doerks T., Braun I.C., Sattler M., Izaurralde E., Bork P.;
 RT "Prediction of structural domains of TAP reveals details of its
 RT interaction with p15 and nucleoporins.";
 RL EMBO Rep. 1:53-58(2000).
 RN (11)
 RP INTERACTION WITH THOC4 AND THE EXON JUNCTION COMPLEX.
 RX MEDLINE=21564074; PubMed=11707413;
 RA Kataoka N., Drem M.D., Kim V.N., Yong J., Dreyfuss G.;
 RT "Magoh, a human homolog of Drosophila mago nashi protein, is a
 RT component of the splicing-dependent exon-exon junction complex.";
 RL EMBO J. 20:6424-6433(2001).
 RN (12)
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 102-372.
 RX MEDLINE=20514125; PubMed=11060011;
 RA Liker E., Fernandez E., Izaurralde E., Conti E.;
 RT "The structure of the mRNA export factor TAP reveals a cis arrangement
 RT of a non-canonical RNP domain and an LRR domain.";
 RL EMBO J. 19:5587-5598(2000).
 RN (13)
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF COMPLEX WITH NXT1, AND X-RAY
 RP CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF COMPLEX WITH NXT1-FG-REPEAT.
 RX MEDLINE=21468398; PubMed=11583626;
 RA Fribourg S., Braun I.C., Izaurralde E., Conti E.;
 RT "Structural basis for the recognition of a nucleoporin FG repeat by
 RT the NTF2-like domain of the TAP/p15 mRNA nuclear export factor.";
 RL Mol. Cell 8:645-656(2001).
 RN (14)
 RP X-RAY CRYSTALLOGRAPHY (1.0 ANGSTROMS) OF 561-619 IN COMPLEX WITH
 RP RANBP3.
 RX MEDLINE=22469929; PubMed=12581645;
 RA Grant R.P., Neuhaus D., Stewart M.;
 RT "Structural basis for the interaction between the Tap/NXF1 UBA domain
 RT and FG nucleoporins at 1A resolution.";
 RL J. Mol. Biol. 326:849-858(2003).
 RN (15)
 RP STRUCTURE BY NMR OF 551-619, AND MUTAGENESIS OF PHE-617.
 RX MEDLINE=21912422; PubMed=11875519;
 RA Grant R.P., Hurt E., Neuhaus D., Stewart M.;
 RT "Structure of the C-terminal FG-nucleoporin binding domain of
 RT Tap/NXF1.";
 RL Nat. Struct. Biol. 9:247-251(2002).
 CC -!- FUNCTION: Involved in the nuclear export of mRNA species bearing
 CC retroviral constitutive transport elements (CTE) and in the export
 CC of mRNA from the nucleus to the cytoplasm.
 CC -!- SUBUNIT: Interacts with NXT1, NXT2, E1B-AP5, RAE1, THOC4
 CC and with several nucleoporins. Is part of the exon
 CC junction complex (EJC) containing NCBP1, NCBP2, RNPS1, RNPSA,
 CC SRRM1, NXF1, NXF2, UPF3B, UPF2 and THOC4.
 CC -!- SUBCELLULAR LOCATION: Nuclear; localized predominantly in the
 CC nucleoplasm and at both the nucleoplasmic and cytoplasmic faces of
 CC the nuclear pore complex. Shuttles between the nucleus and the
 CC cytoplasm.
 CC -!- TISSUE SPECIFICITY: Expressed ubiquitously.
 CC -!- DOMAIN: The minimal CTE binding domain consists of an RNP-
 CC type RNA binding domain (RBD) and leucine-rich repeats.
 CC -!- DOMAIN: The nucleoporin binding domain consists of a NTF2-like
 CC domain and a UBA-like domain. The NTF2 domain heterodimerizes with
 CC NXT1 and NXT2. The formation of NXF1/NXT1 heterodimers is required
 CC for NXF1-mediated nuclear mRNA export. The UBA-like domain
 CC mediates direct interactions with nucleoporin-FG-repeats and is
 CC necessary and sufficient for localization of NXF1 to the nuclear
 CC rim. The conserved loop 594-NWD-596 of the UBA domain has a
 CC critical role in the interaction with nucleoporins.
 CC -!- DOMAIN: The leucine-rich repeats and the NTF2-domain are
 CC essential for the export of mRNA from the nucleus.
 CC -!- MISCELLANEOUS: The RNA-binding domain is a non-canonical RNP-type
 CC domain.
 CC -!- SIMILARITY: Belongs to the NXF family.
 CC -!- SIMILARITY: Contains 4 leucine-rich (LRR) repeats.
 CC -!- SIMILARITY: Contains 1 NTF2 domain.
 CC -!- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
 CC -!- SIMILARITY: Contains 1 UBA-like domain.
 CC -----
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CC -----

DR EMBL; AJ132712; CAA10753.1; -

DR EMBL; AF112880; AAD39102.1; -

DR EMBL; AF126246; AAD20016.1; -

DR EMBL; AK027192; -; NOT_ANNOTATED_CDS.

DR EMBL; BC004904; AAH04904.1; -

DR EMBL; BC028041; AAH28041.1; -

DR EMBL; EU00073; AAB11111.1; -

DR PDB; 1FOI; 03-NOV-00.

DR PDB; 1FT8; 11-DEC-00.

DR PDB; 1KOH; 27-FEB-02.

DR PDB; 1KOO; 27-FEB-02.

DR PDB; 1OAI; 20-FEB-03.

DR Genew; HGNC:8071; NXF1.

Query Match 7.6%; Score 93; DB 1; Length 619;
Best Local Similarity 24.7%; Pred. No. 0.65;
Matches 60; Conservative 32; Mismatches 93; Indels 58; Gaps 13;

QY 5 AGDSGML-----ACLCITLWHLPAVPAALNETGDP-GPGPSIQKTYDLT---RYLEHQL 54

Db 400 SGRQGLLDAYHDGACCSLSIFIFQNPAPSSLAIFYKDSRVKXKDKPTLFRLLKXTR 459

QY 55 RSLAGTYLNYLGGPFNEPDPNP--PRLGAETLPRATVDL-----EVRSLNDKUR-LTON 106

Db 460 LNVV-AFLNEL--PKTQHDVNSFVVDISAQSTLLCFSGVNGVFKEVDGKSRDSLAFAFTR 516

QY 107 Y---EAYSHLLCYLRG--LNROAATAELERSLAHFTCTSLQGLGSIAGVMAALGYPLPOP 161

Db 517 FIAPVPSNGLCIVNDELFRVNASSEEIOAFA-----WPAF 553

QY 162 LPQTEPTWPGPAHSDFLQK-----MDDFWLLKELQTLW-----RSKDFNRLKKMQPP 212

Db 554 TFSSTVPITLSPQEQMLQAFSTQSGMNLWSQKCLQDNWDYTRSAQAFTHLAKAKGIP 613

QY 213 AAA 215

Db 614 EVA 616

RESULT 7

ID	CTFL_HUMAN	STANDARD;	PRT;	201 AA.
AC	Q16619;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Cardiotrophin-1 (CT-1).			
GN	CTFL.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Heart;			
RX	MEDLINE=96429882; PubMed=8833032;			
RA	Pennica D., Swanson T.A., Shaw K.J., Kuang W.-J., Gray C.L.,			
RA	Beatty B.G., Wood W.I.;			
RT	"Human cardiotrophin-1: protein and gene structure, biological and			
RT	binding activities, and chromosomal localization.";			
RL	Cytokine 8:183-189(1996).			
CC	-1- FUNCTION: Induces cardiac myocyte hypertrophy in vitro. Binds to			
CC	and activates the IL6/gp130 receptor.			
CC	-1- SUBCELLULAR LOCATION: Secreted.			
CC	-1- TISSUE SPECIFICITY: Highly expressed in heart, skeletal muscle,			
CC	prostate and ovary. Lower levels in lung, kidney, pancreas,			
CC	thymus, testis and small intestine. Little or no expression in			
CC	brain, placenta, liver, spleen, colon or peripheral blood			
CC	leukocytes.			
CC	-1- SIMILARITY: Belongs to the IL-6 superfamily.			

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CC -----

DR EMBL; U43033; AAD12173.1; -

DR EMBL; U43031; AAD12173.1; JOINED.

DR EMBL; U43032; AAD12173.1; JOINED.

DR EMBL; U43030; AAB85229.1; -

DR PIR; G02312; G02312.

DR Genew; HGNC:2499; CTF1.

DR MIM; 600435; -

DR GO; GO:0005576; C:extracellular; TAS.

DR GO; GO:0005146; P:leukemia inhibitory factor receptor binding; TAS.

DR GO; GO:0008283; P:cell proliferation; TAS.

DR GO; GO:0007267; P:cell-cell signaling; TAS.

DR GO; GO:0007517; P:muscle development; TAS.

DR GO; GO:0007399; P:neurogenesis; TAS.

DR GO; GO:0008284; P:positive regulation of cell proliferation; TAS.

KW Cytokine; Polymorphism.

FT VARIANT 92 92 A -> T (in dbSNP:2234933).

FT /FTID=VAR_014938.

SQ SEQUENCE 201 AA; 21227 MW; 0235A7B5745F675F CRC64;

Query Match 7.5%; Score 91.5; DB 1; Length 201;
Best Local Similarity 25.9%; Pred. No. 0.21;
Matches 45; Conservative 24; Mismatches 92; Indels 13; Gaps 5;

QY 40 IQTYDLTRYLEHQLSLAGTYLNYLGGPFNEPDPNPRLGAETLPRATVDLEWRLND 99

Db 27 IROTSHLHLLTKYASQLQEQYVQLQDFGDFGDFGDFGDFGDFGDFGDFGDFGDFGDF 85

QY 100 KLRLTQNEYAYSHLLCYLRGLNRQAA-----TAELEERSLAHFTCTSLQGLGSIAGVMAAL 154

Db 86 RLRL--DAALALPPLLDVACRRQALNPAPRLRLRLRLRLRLRLRLRLRLRLRLRLRL 143

QY 155 GYPLPQPLPQTEP---TWTFGPAHSDFLQKMDDFWLLKELQTLWLSAKDFNRL 205

Db 144 G--AANRGPRAEPPEAATASASATGVPAKVLGLRVGLYREWLSTRTGDLGL 195

RESULT 8

ID	HAIR_MOUSE	STANDARD;	PRT;	1182 AA.
AC	Q61645; Q80V47;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	10-OCT-2003 (Rel. 42, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Hairless protein.			
GN	HR.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Balb/c; TISSUE=Skin;			
RX	MEDLINE=94329587; PubMed=8052649;			
RA	Cachon-Gonzalez M.B., Fenner S., Coffin J.M., Moran C., Best S.,			
RA	Stoye J.P.;			
RT	"Structure and expression of the hairless gene of mice.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 91:7717-7721(1994).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6; TISSUE=Retina;			
RX	MEDLINE=22388257; PubMed=12477932;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra V.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: May act as a transcription factor that could act on to
CC regulate one of the phases of hair growth.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- TISSUE SPECIFICITY: Expressed predominantly in brain, hair
CC follicles and interfollicular epidermis. No expression in
CC dermis.
CC -!- DISEASE: HR MUTATION PRODUCES A NUMBER OF PLEIOTROPIC EFFECTS
CC INCLUDING STRUCTURAL ABNORMALITIES OF EPITHELIAL CELLS IN THE HAIR
CC FOLLICLES, HAIR LOSS TOWARDS THE END OF THE FIRST HAIR GROWTH
CC CYCLE, AND THE FAILURE OF SUBSEQUENT HAIR GROWTH CYCLES. OLDER
CC MICE CARRYING AN HR MUTATION HAVE BEEN REPORTED TO POSSESS ALTERED
CC RATIOS OF T-CELL-DEPENDENT B-CELL RESPONSES. MICE HOMozyGous FOR
CC HR MUTATION ARE UNIQUELY SENSITIVE TO UV AND CHEMICALLY INDUCED
CC SKIN TUMORS.
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CC -----
CC EMBL; 232675; CA83587.1; -;
CC EMBL; BC049182; RAH49182.1; -;
CC PIR; I48378; I48378.
CC MGD; MGI:96223; hr.
CC InterPro; IPR003347; TF_JmJC.
CC Pfam; PFO2373; JmJC; 1.
CC SMART; SM00558; JmJC; 1.
CC Zinc-finger; DNA-binding; Nuclear protein; Transcription regulation;
CC Metal-binding
CC ZN_FING 595 620 C6-TYPE.
CC DOMAIN 535 540 POLY-GLY.
CC CONFLICT 401 401 P -> S (IN REF. 1).
CC SEQUENCE 1182 AA; 127192 MW; 3AFABE96C6EB3241 CRC64;
CC -----
CC Query Match 7.5%; Score 91.5; DB 1; Length 1182;
CC Best Local Similarity 23.7%; Pred. No. 2;
CC Matches 70; Conservative 25; Mismatches 99; Indels 101; Gaps 17;
CC
CC 3 LRAGDSWGMGLACTVLMWHLPAVPAALNRTGPG-----PGP----- 38
CC 813 LRAGS-----GLRGL-----SLPLSPVRLTSLPPGALLMLOEPRPKHGPHLPOEHWRCQPV 865
CC 39 ---STQTYDLYRLEHQRLSLAGTY---LNYLGGP-----FNEPDPNPPRLG 80
CC 866 LVSGGQKTLRLSLWMEALGTGGVOTLTALGPPQPTNLDSFAWEGFSHPETRP----- 921
CC 81 AETLPRAVTDVLEWVRSNDK-LRLTQN-----YEAYSHLLCYL-RGLNRQAAT 126
CC 922 --KLDEGSV-LLHRTLGDKASRQNLASSLPPEYCAHQGKLNLSYLPGLTLPLE 978
CC 127 AEL-----RRSLAHFCTSLQGLLGSIAAGMALGYPLPQLPGTEPTWTPGPAH 175
CC 979 FQLWAAYGVNGHRGHLGKFNLCVEVSDLSILVHAEAL-----PPWY--RAQ 1024

QY 176 SDFLQKMD--DFWLLKEQLTWLWR--SAKDNLRLKKMQP--PAAAVTLHLGHHG 224
Db 1025 KDFLSGLDGEGLSPGSGTSTVWHVFRQAQRIIRFLQWVCPAGAGTLEPGAPG 1079

RESULT 9

CNTF_CHICK
ID CNTF_CHICK STANDARD; PRT; 195 AA.
AC Q02011;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Ciliary neurotrophic factor (CNTF) (Growth promoting activity) (GPA).
GN CNF OR GPA.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92304573; PubMed=1610564;
RA Leung D.W., Parent A.S., Cachianes G., Lee A.L., Nikolic K.,
RA Esch F., Coulombe J.N., Blacher R.W., Eckenstein F.P., Nishi R.;
RT "Cloning, expression during development, and evidence for release of
RT a trophic factor for ciliary ganglion neurons.";
RL Neuron 8:1045-1053(1992).
CC -!- FUNCTION: CNTF is a survival factor for various neuronal cell
CC types. Seems to prevent the degeneration of motor axons after
CC axotomy.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- TISSUE SPECIFICITY: Nervous system.
CC -!- SIMILARITY: Belongs to the CNTF family.
CC -----
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CC -----
CC EMBL; M80827; AAA48784.1; -;
CC PIR; JH0680; JH0680.
CC HSP; P26441; 1CNT.
CC InterPro; IPR000151; Ctl_neuro_factor.
CC Pfam; PFO1110; CNTF; 1.
CC ProDom; PD011041; Ctl_neuro_factor; 1.
CC KW Growth factor; Neurone.
CC SEQUENCE 195 AA; 21330 MW; FEA07694DB344CS CRC64;
CC -----

Query Match 7.4%; Score 91; DB 1; Length 195;
Best Local Similarity 27.3%; Pred. No. 0.23;
Matches 51; Conservative 21; Mismatches 83; Indels 32; Gaps 9;

QY 46 LTRYLEHQRLSLAGTYLNYLGGPDPNPPRLGAEATLPRAVTDVLEWVRSNDKRLRLTQ 105
Db 23 LARKMSDVTDLDDIYVERQG-----LDASISVAADVGVPTAAV--ERWAEQTGTQLLD 75
QY 106 N----YEAYSHLLCYLRLNRQA---ATAELRSLA-----HFTSLQGLLGSIAGVMA 152
Db 76 NLAAVEAFRTLLAQMLEEQRELIGDTPDALGPAALMLQVSAFVYHLELL-----ELE 130
QY 153 ALGYPLPQPLPGTEPTWTPGPAH--SDFLOKMDDFWLLKEQLTWLRSADKFNRLKKMQP 211
Db 131 SRGAPAE---GSEP---PAPPLSLFEQKRLGLVRLRLAQWAVRSVRDLRLSKHGPG 184
QY 212 PAAAVTL 218
Db 185 SGAALGL 191


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RESULT 10
MIP1_SCHPO STANDARD; PRT; 1313 AA.
AC P97141;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE WD-repeat protein mipl.
GN MIP1 OR SPAC57A7.11.
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A., FUNCTION, AND SUBCELLULAR LOCATION.
RX MEDLINE=20115869; PubMed=10648609;
RA Shinozaki-Yabana S., Watanabe Y., Yamanoto M.;
RT "Novel WD-repeat protein Mip1p facilitates function of the meiotic
RL Mol. Cell. Biol. 20:1234-1242(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Ocell J.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squires R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Art R., Robben J., Gymnopoulos B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl M., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Moreno S., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Lowe T., Armstrong J., Forsburg S.L.,
RA Cerretti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrett B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe."
RL Nature 415:871-880(2002).
CC [1]- FUNCTION: BINDS TO AND FACILITATES THE FUNCTIONING OF THE MEIOTIC
CC REGULATOR MEI2. MAY ALSO BE INVOLVED IN CONJUGATION BY INTERACTING
CC WITH STE11. ESSENTIAL FOR CELL GROWTH.
CC [2]- SUBCELLULAR LOCATION: Cytoplasmic.
CC [3]- SIMILARITY: Contains 7 WD repeats.
CC
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CC
CC EMBL; AB032552; BAA84585.1;
CC EMBL; Z55396; CAB08769.1;
CC PIR; T38943;
CC GeneDB SPombe; SPAC57A7.11;
CC InterPro; IPR008938; ARM.
CC InterPro; IPR001680; WD40.
CC InterPro; IPR004083; Yeast176.
CC Pfam; PF00400; WD40; 5.

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PRINTS; PRO1547; YEAST176DUF.
DR SMART; SMO0320; WD40; 6.
DR PROSITE; PS00678; WD_REPEATS_1; 1.
DR PROSITE; PS00682; WD_REPEATS_2; 2.
DR PROSITE; PS0294; WD_REPEATS_REGION; 1.
KW Metosis; WD repeat; Repeat.
FT REPEAT 986 1029 WD 1.
FT REPEAT 1033 1074 WD 2.
FT REPEAT 1087 1126 WD 3.
FT REPEAT 1130 1170 WD 4.
FT REPEAT 1176 1216 WD 5.
FT REPEAT 1219 1259 WD 6.
FT REPEAT 1268 1308 WD 7.
SQ SEQUENCE 1313 AA; 148533 MW; C71B663B0171E7A4 CRC64;

Query Match 7.3%; Score 89.5; DB 1; Length 1313;
Best Local Similarity 22.8%; Pred.No.3.6;
Matches 61; Conservative 32; Mismatches 69; Indels 105; Gaps 14;

QY 15 ICTVLMHLPV--PALNR-----TGDPGPGPSI-----QKTYDLTRYLEHQLRS 56
DB 811 LAFLLQHLPALHKASLSDTNSVSDPKPHFVPSVSENKILNRSFSLTRSLKGLALS 870
QY 57 LAG-----TVLYNL-----GPP-FNEPDPNPRLGAETUPRATVDL 91
DB 871 LAGSDRASSELLNGENKPAESNLNHLTSAKVPGPPAFNELEY-----QSELD 919
QY 92 EVWSRLND-----KLRLTONYEAYSHLLCYLRLG---NRQAATAELRRSLAHEFCTS 139
DB 920 PLTSYLFDSWRKYFTPEQNPNEDEFGS--ICYNQLWRNRNEKLIYTRPLAEYSTN 977
QY 140 -----LQGLIGSAGVMAALGYPLPQLPTEFTPTPGFAHSDFLQMDDFWLLKE--- 190
DB 978 GRWNQQLMTFNNTA-----PRKLMFHQFEDQLITLGDKI 1013
QY 191 LQTVLWRSKADFNELKKKMQPPAAAVT 217
DB 1014 IQVWDWR-----NRCLNSFKTSASATT 1036

RESULT 11
HAIR_RAT
ID HAIR_RAT STANDARD; PRT; 1181 AA.
AC P97609;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Hairless protein.
GN HR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=97141510; PubMed=8987811;
RA Thompson C.C.;
RT "Thyroid hormone-responsive genes in developing cerebellum include a
RL J. Neurosci. 16:7832-7840(1996).
CC [1]- FUNCTION: May act as a transcription factor that could act on to
CC regulate one of the phases of hair growth.
CC [2]- SUBCELLULAR LOCATION: Nuclear.
CC
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CC

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DR EMBL; U71293; AAC53018.1; ALT INIT.
 DR InterPro; IPR003347; TF_JmJC.
 DR Pfam; PF02373; JmJC; 1.
 DR SMART; SM00558; JmJC; 1.
 KW Zinc-finger; DNA-binding; Nuclear protein; Transcription regulation;
 FT Metal-binding.
 ZN_FING 594 619 C6-TYPE.
 SQ SEQUENCE 1181 AA; 127307 MW; 83457029CF8E88F0 CRC64;

Query Match 7.1%; Score 87.5; DB 1; Length 1181;
 Best Local Similarity 25.3%; Pred. No. 4.8;
 Matches 61; Conservative 21; Mismatches 92; Indels 67; Gaps 12;

QY 30 RTGDPGPGPSIQKTYLDTRYLEHQLRSAGTY--LNYLGPP-----FNPPDF 74
 Db 859 RQGVVLVSGIQKTLRLSLWGMEALTLGGVQVTLTALGPQPTSLDSTAFKWFSPHEA 918
 QY 75 NPPLRGAETLPATVDLEWVSLNDK-----LRLTQ-----NRYAYSHLLC 115
 Db 919 RP-----KLDEGVS-LTLHRRPLGDKDSRVENASSLPPEYCAHQGKLNLASYPGL 971
 QY 116 YLRGLNRQAATAELRRS-----LAHFCTSLQGLLGSAGVMAALGYPLPQPLPCTPTW 169
 Db 972 TLHPLPQLWAAYGVNSRHGLTKNLVVEYSDLSILVHAEAQ-----PPW 1019
 QY 170 TPGPAHSDFLOKMD--DFWLLKELQTLWR--SAKDFNRLKKMQP--PAAAVTLHLGAH 223
 Db 1020 Y--RAQDFLSGLDGEGLWSPGQSQTSTVHVFRQAQRIIRFLQWVCPAGAGTLFPGAP 1077
 QY 224 G 224
 Db 1078 G 1078

RESULT 12
 M2B2 HUMAN
 ID M2B2 HUMAN STANDARD; PRT; 1009 AA.
 AC Q9V3E5;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DE Epididymis-specific alpha-mannosidase precursor (BC 3.2.1.24)
 DE (Mannosidase alpha class 2B member 2).
 GN MAN2B2 OR KIAA0935.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Stone N.E., Schmutz J.J., Cox D.R., Myers R.M.;
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 132-1009 FROM N.A.
 RA TISSUE=Brain;
 RC MEDLINE=99246063; PubMed=10231032;
 RA Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hirose M.,
 RA Miyajima N., Tanaka A., Kori H., Nomura N., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. XIII.
 RT The complete sequences of 100 new cDNA clones from brain which code
 RL for large proteins in vitro.";
 RL DNA Res. 6:63-70(1999).
 RN [3]
 RP RECONSTRUCTION FROM GENOMIC SEQUENCE.
 RA Bairoch A.;
 RL Unpublished observations (NOV-2001).
 CC -!- CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing alpha-D-
 CC mannose residues in alpha-D-mannosides.
 CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
 CC -!- SIMILARITY: Belongs to family 38 of glycosyl hydrolases.
 CC -----
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 CC -----
 DR EMBL; AC004480; -; NOT ANNOTATED CDS.
 DR EMBL; AB023152; BAA76779.1; ALT SEQ.
 DR InterPro; IPR000602; Glyco_hydro_38.
 DR Pfam; PF01074; Glyco_hydro_38; 1.
 KW Hydrolase; Glycosidase; Signal; Glycoprotein.
 FT SIGNAL 1 23 POTENTIAL.
 FT CHAIN 24 1009
 FT CARBOHYD 226 226 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 249 249 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 294 294 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 336 336 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 516 516 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 608 608 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 670 670 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 748 748 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 808 808 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 812 812 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 890 890 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 1009 AA; 113987 MW; F3DB81DD061352E6 CRC64;

Query Match 7.0%; Score 86; DB 1; Length 1009;
 Best Local Similarity 23.3%; Pred. No. 5.5;
 Matches 45; Conservative 20; Mismatches 66; Indels 62; Gaps 8;

QY 50 LEHQ----LRSLAGTYLNYLGGPFNPPRLGAEITLPATVDLEWVRSNDKRLTQ 105
 Db 842 LQHRPVVFLGDLAGTAPKLPGPQQQEAATLPFNLHLQIL-----SIPGWRYSNHTHSQ 896
 QY 106 NYEAYSHLLCYLRGLNRQAATAELRS LAHF-----CTSLQGLLGSAG 149
 Db 897 N-----LRKGRGGEAQADRLRLRLVHLYVEGEDPVLSPQVTNVLQAVLOAGS 946
 QY 150 VMAALGYPLPQPLPQPTGTEPTWTEGPAHSDFLOKMDDFWLLKELQTLWVRSNDKRLTQ 207
 Db 947 VVAV----EERSLTGT-----WDLMSLHRSWRTGPGHRGDTTS 982
 QY 208 KMOPPA-AVTLH 219
 Db 983 PSRPPGPGPIITVH 995

RESULT 13
 PHAC_PSEOL
 ID PHAC_PSEOL STANDARD; PRT; 560 AA.
 AC P26496;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Poly(3-hydroxyalkanoate) polymerase 2 (EC 2.3.1.-) (PHA polymerase 2)
 DE (PHA synthase 2) (Polyhydroxyalkanoic acid synthase 2).
 GN PHAC.
 OS Pseudomonas oleovorans.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=301;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GP01;
 RX MEDLINE=91115930; PubMed=1989978;
 RA Huisman G.W., Wouink E., Meima R., Kazemier B., Terpstra P.,
 RA Witholt B.;
 RT "Metabolism of poly(3-hydroxyalkanoates) (PHAs) by Pseudomonas
 RT oleovorans: Identification and sequences of genes and function of the
 RT encoded proteins in the synthesis and degradation of PHA.";
 RL J. Biol. Chem. 266:2191-2198(1991).
 CC -!- FUNCTION: P.OLEOVORANS ACCUMULATES POLY(3-HYDROXYALKANOATES) AFTER

CC GROWTH ON MEDIUM CHAIN LENGTH HYDROCARBONS. LARGE AMOUNTS OF THIS
CC POLYESTER ARE SYNTHESIZED WHEN CELLS ARE GROWN UNDER NITROGEN-
CC LIMITING CONDITIONS. WHEN NITROGEN IS RESUPPLIED IN THE MEDIUM,
CC THE ACCUMULATED PHA IS DEGRADED.
CC -1- SIMILARITY: Belongs to the PHA/PHB synthase family.
CC
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CC
CC EMBL; M58445; AAA5934.1; --
CC PIR; C38604; C38604.
CC InterPro; IPR000073; A/b hydrolase.
CC Pfam; PF00561; abhydrolase; 1.
CC PHA biosynthesis; Transferase; Acyltransferase.
CC ACT SITE 296 296 POTENTIAL
CC SEQUENCE 560 AA; 62631 MW; E2CD844FC1616B83 CRC64;
CC
CC Query Match 7.0%; Score 85.5; DB 1; Length 560;
CC Best Local Similarity 30.2%; Pred. No. 2.9;
CC Matches 38; Conservative 17; Mismatches 42; Indels 29; Gaps 7;
CC
CC 77 PRGAEPLPRATVDLEWRSNDKRLKLTQNYEAYSHLLCYLRGLNRQAATAELRRSL--A 134
CC 5 PAKGTPTLPATSKVQ-----NAILGRG-----DLSTLRNVSRQS-----LRPLHTA 50
CC
CC 135 HFCTSLQGLIGSIAGVMAALGYPLPQPG-----TEPTWPGPAHSDFLQKMDDFWLLKE 190
CC 51 HHLALGGQLGRV-----ILGDTPLQPNRDRPSDPTWSQNPFRYRGLQA-----YLAQ 101
CC
CC 191 LQTWLV 196
CC 102 KQTRLV 107
CC
CC RESULT 14
CC CNTF_PIG STANDARD; PRT; 200 AA.
CC AC 002732;
CC DT 15-JUL-1998 (Rel. 36, Created)
CC DT 15-JUL-1998 (Rel. 36, Last sequence update)
CC DT 30-MAY-2000 (Rel. 39, Last annotation update)
CC DE Ciliary neurotrophic factor (CNTF).
CC GN
CC OS Sus scrofa (Pig).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
CC OX NCBI_TaxID=9823;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RX MEDLINE=98030048; PubMed=9363597;
CC RA Weaks R.L., Ramsoondar J.J., Gallagher D.S. Jr., Nogues C.,
CC Predahl J.A.;
CC RT "Isolation, characterization and chromosomal localization of the
CC porcine ciliary neurotrophic factor (CNTF) gene."
CC RL Anim. Genet. 28:354-357(1997).
CC CC -1- FUNCTION: CNTF is a survival factor for various neuronal cell
CC types. Seems to prevent the degeneration of motor axons after
CC axotomy (By similarity).
CC CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC CC -1- TISSUE SPECIFICITY: Nervous system (By similarity).
CC CC -1- SIMILARITY: Belongs to the CNTF family.
CC
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CC
CC EMBL; U57644; AAC27342.1; --
CC HSP; P28441; ICNT.
CC InterPro; IPR000151; Ctl_neuro_factor.
CC Pfam; PF01110; CNTF; 1.
CC ProDom; PD011041; Ctl_neuro_factor; 1.
CC KW Growth factor; Neurone.
CC SEQUENCE 200 AA; 22718 MW; 40507C4457ED6531 CRC64;
CC
CC Query Match 6.9%; Score 84; DB 1; Length 200;
CC Best Local Similarity 24.7%; Pred. No. 1.1;
CC Matches 47; Conservative 23; Mismatches 88; Indels 32; Gaps 9;
CC
CC 46 LTRYLEHQLRSLAGTYLNLGPPFPDFNPPLRGAETLPRAVTVLEWRSNDKRLKLTQ 105
CC 23 LARKIRSDLTALMEAYVKGQ--LNE---NINLSDVDGVPMASDR--HSELTEAERLQE 75
CC 106 NYEAYSHLLCYLRGLNRQAATAELRRSLAHFCTS-----LQGLIGSIAGVMAALGYPLPQ-- 160
CC 76 NLRAVTRTFHVLARL-----LEDQREHFTPAEDDFHQAIIHTIVLQVAAFAFYQLEELM 127
CC
CC 161 -----PLPGTEPTWPGPAHSD--FLQKMDDFWLLKEQTLWRSAXDFNRLKKKQPPA 213
CC 128 VLLEHKVPPSEADGTPLSVGGGLFEKKLWGLKVLQELSQWTVRSRDLRVISSHQ----- 183
CC
CC 214 AAVTLHLGAH 223
CC 184 AGVPAH-GSH 192
CC
CC RESULT 15
CC TLL_DROME STANDARD; PRT; 452 AA.
CC ID TLL_DROME
CC AC P18102; Q9VA33;
CC DT 01-NOV-1990 (Rel. 16, Created)
CC DT 01-NOV-1990 (Rel. 16, Last sequence update)
CC DT 10-OCT-2003 (Rel. 42, Last annotation update)
CC DE Tailless protein.
CC GN TLL OR NR2B2 OR CG1378.
CC OS Drosophila melanogaster (Fruit fly).
CC OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
CC OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
CC OC Ephydroidea; Drosophilidae; Drosophila.
CC OX NCBI_TaxID=7227;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RC STRAIN=Oregon-R;
CC RX MEDLINE=90304905; PubMed=2364433;
CC RA Pignoni F., Baldairelli R.M., Steingrimsson E., Diaz R.J.,
CC Patapoutian A., Merriam J.R., Lengyel J.A.;
CC RT "The Drosophila gene tailless is expressed at the embryonic termini
CC and is a member of the steroid receptor superfamily."
CC RL Cell 62:151-163(1990).
CC RN [2]
CC RP SEQUENCE FROM N.A.
CC RX MEDLINE=93157371; PubMed=8430097;
CC RA Liaw G.-J., Steingrimsson E., Pignoni F., Courcy A.J., Lengyel J.A.;
CC RT "Characterization of downstream elements in a Raf-1 pathway."
CC RL Proc. Natl. Acad. Sci. U.S.A. 90:858-862(1993).
CC RN [3]
CC RP SEQUENCE FROM N.A.
CC RC STRAIN=Berkely;
CC RX MEDLINE=20196006; PubMed=10731132;
CC RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
CC Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
CC George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
CC Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
CC Brandon R.C., Rogers Y.-H.C., Blazer V.G., Champ M., Pfeiffer B.D.,
CC Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,
CC Abrell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
CC Balley R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
CC Beeson K.V., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

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DR HSP; P10826; IHRA.
DR TRANSFAC; T00789; -.
DR FlyBase; FBgn0003720; t11.
DR GO; GO:0004579; F:ligand-dependent nuclear receptor activity; NAS.
DR GO; GO:0007369; P:gastrulation; NAS.
DR GO; GO:0007362; P:terminal region determination; IGI.
DR GO; GO:0008293; P:torso signaling pathway; IGI.
DR GO; GO:0006351; P:cis transcription, DNA-dependent; NAS.
DR InterPro; IPR000536; Hormone rec lig.
DR InterPro; IPR001723; Sterhorm receptor.
DR InterPro; IPR008946; Str ncl_receptor.
DR InterPro; IPR001628; Znf_C4steroid.
DR Pfam; PF00134; hormone_rec; 1.
DR Pfam; PF00105; zf-C4; 1.
DR PRINTS; PR00398; STRDHORMONER.
DR PRINTS; PR00047; STROIDFINGER.
DR ProDom; PD000035; Znf_C4steroid; 1.
DR SMART; SM00430; HOLI-1.
DR SMART; SM00399; ZNF_C4; 1.
DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
DR KW Receptor; Transcription regulation; DNA-binding; Nuclear protein;
KW Zinc-finger; Activator; Repressor; Developmental protein.
FT DNA_BIND 34 101 NUCLEAR RECEPTOR-TYPE.
FT ZN_FING 34 54 C4-TYPE.
FT ZN_FING 70 96 C4-TYPE.
FT DOMAIN 244 389 LIGAND-BINDING (BY SIMILARITY).
FT DOMAIN 262 265 POLY-LEU.
SQ SEQUENCE 452 AA; 50549 MW; A4ABEFFDE993A37C CRC64;

Query Match 6.8%; Score 83; DB 1; Length 452;
Best Local Similarity 23.8%; Pred No 3.8;
Matches 34; Conservative 11; Mismatches 32; Indels 66; Gaps 67

QY 115 CYLRGLNRQANTAE-----LRRSLAHFCTSLQGLGSIAGVM-----AALG 155
Db 96 CFEVGNKDAVQHERGPERNSTLRHMVWYKDMWG-----AGEMFQIPAEILMTAALTG 150
QY 156 YP-LPQPLPCTETFTPGPAHSDFLQKMDDFLLKELQTLWRSKDFNRLLKXKQSPAA 214
Db 151 FPGVPMPEPLQPORAGHPAHMAFQ-----PPPSA 181
QY 215 AVTL-----HLGAHF 225
Db 182 AAVLDLSVPRVPHHPVHQHGPF 204

Search completed: August 10, 2004, 06:46:26
Job time : 10 secs

```


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OM protein - protein search, using sw model

Run on: August 10, 2004, 06:43:28 ; Search time 35 Seconds
(without alignments)

2028.331 Million cell updates/sec

Title: US-09-931-704-2

Perfect score: 1226

Sequence: 1 MDLRAGDSWGLACICTVLW.....KKMQPPAAAVTLHLGAHGF 225

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 1000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mnc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1226	100.0	225	4 Q9UBD9	Q9ubd9 homo sapien
2	1193	97.3	225	11 Q9Q2M3	Q9qzm3 mus musculu
3	150.5	12.3	215	13 Q9PUU1	Q9puj1 plethodon j
4	150.5	12.3	215	13 Q9PUU0	Q9puj0 plethodon j
5	150.5	12.3	215	13 Q9PUU2	Q9puj2 plethodon j
6	148.5	12.1	215	13 Q9PUU9	Q9puj9 plethodon j
7	105	8.6	471	16 Q9BAR4	Q9bar4 pseudomonas
8	97.5	8.0	318	4 Q96LS2	Q96ls2 homo sapien
9	97.5	8.0	530	3 Q8X0E9	Q8x0e9 neurospora
10	97	7.9	8601	2 Q8GM87	Q8gm87 symbiont ba
11	96.5	7.9	243	4 Q8NEV9	Q8nev9 homo sapien
12	94	7.7	287	4 Q8N358	Q8n358 homo sapien
13	93	7.6	392	2 Q8KNF2	Q8knf2 micromonosp
14	92.5	7.5	860	16 Q82G16	Q82g16 streptomyce
15	92	7.5	332	10 Q9MAU1	Q9mau1 arabidopsis
16	91.5	7.5	716	16 Q8P199	Q8p199 xanthomonas

ALIGNMENTS

RESULT 1

Q9UBD9 PRELIMINARY; PRT; 225 AA.

AC Q9UBD9;

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)

DE Neurotrophin-1/B-cell stimulating factor-3 (Cardiotrophin-like

DE cytokine) (Similar to cardiotrophin-like cytokine, neurotrophin-1/B-cell stimulating factor-3).

GN CLC.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP MEDLINE=99433254; PubMed=10500198;

RA Senaldi G., Varnum B.C., Sarmiento U., Starnes C., Lile J., Scully S.,

RA Guo J., Elliott G., McNinch J., Shaklee C.L., Freeman D., Manu F.,

RA Simonet W.S., Boone T., Chang M.-S.;

RT "Novel neurotrophin-1/B cell-stimulating factor-3: A cytokine of the

RT IL-6 family."

RL Proc. Natl. Acad. Sci. U.S.A. 96:11458-11463(1999).

RN [2]

RP SEQUENCE FROM N.A.

RA MEDLINE=99382254; PubMed=10448081;

RA Shi Y., Wang W., Yourey P.A., Gohari S., Zukauskas D., Zhang J.,

RA Ruben S., Alderson R.F.;

RT "Computational EST database analysis identifies a novel member of the

RT neurotrophic cytokine family."

RL Biochem. Biophys. Res. Commun. 262:132-138(1999).

RN [3]

RP SEQUENCE FROM N.A.

RA Hu X., Xu Y., Zhang B., Peng X., Yuan J., Qiang B.;

RL Submitted (JUL-2001) to the EMBL/GenBank/DDAJ databases.

RN [4]

RP SEQUENCE FROM N.A.

RC TISSUE=Kidney;

Q870a3 fusarium ox
Q9s3c9 porphyromon
Q9i664 pseudomonas
Q84n16 zea mays (m
Q8b113 mus musculu
Q8bgr5 mus musculu
Q88287 mus musculu
Q7tsj4 mus musculu
Q88286 mus musculu
Q8krx4 streptomyce
Q54153 streptomyce
Q8hwh4 mus musculu
Q8z1r2 mus musculu
Q8r363 mus musculu
Q88841 mus musculu
Q9cpz1 mus musculu
Q9va71 aeropyrum p
Q8pbb1 brucella me
Q8rx31 brucella su
Q9nxx5 homo sapien
Q9rvf3 deinococcus
Q83432 treponema p
Q8by35 mus musculu
Q9p210 homo sapien
Q82e94 streptomyce
Q9s159 homo sapien
Q88gv1 pseudomonas
Q9rlp6 mycobacteri
Q91584 streptococc

RA Strausberg R.;
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF176912; AAF00992.1; -;
 DR EMBL; AF172854; AADS4284.1; -;
 DR EMBL; AF176911; AAF00991.1; -;
 DR EMBL; AY049779; AAL15436.1; -;
 DR EMBL; BC012939; AAH12939.1; -;
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0005125; F:cytokine activity; NAS.
 DR GO; GO:0019221; P:cytokine and chemokine mediated signaling p...; NAS.
 SQ SEQUENCE 225 AA; 25176 MW; E2DD4B280833B55 CRC64;
 Query Match 100.0%; Score 1226; DB 4; Length 225;
 Best Local Similarity 100.0%; Pred. No. 1.6e-107;
 Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDRAGSWGMLACLTVMHLPALNRTGDPGPGSIQKTYDITRYLEHQLRSLAGT 60
 DB 1 MDRAGSWGMLACLTVMHLPALNRTGDPGPGSIQKTYDITRYLEHQLRSLAGT 60
 QY 61 YLNYLGPPFNEPDPNPRGLGAETLPRAATVLEWRSNDKRLTQNYEAYSHLLCYLRGL 120
 DB 61 YLNYLGPPFNEPDPNPRGLGAETLPRAATVLEWRSNDKRLTQNYEAYSHLLCYLRGL 120
 QY 121 NRQAATAELRSLAHFCTSLQGLLSIAGVMAALGYPLPQPLPGTFTPTWPGFAHSDFLQ 180
 DB 121 NRQAATAELRSLAHFCTSLQGLLSIAGVMAALGYPLPQPLPGTFTPTWPGFAHSDFLQ 180
 QY 181 KMDDFWLLKELQWLRSAKDFNRLKKMQPPAAATVTLHGAHGF 225
 DB 181 KMDDFWLLKELQWLRSAKDFNRLKKMQPPAAATVTLHGAHGF 225
 RESULT 2
 QYQ2M3 PRELIMINARY; PRT; 225 AA.
 AC Q9Q2M3
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Neurotrophin-1/B-cell stimulating factor-3.
 GN BSP3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=9432254; PubMed=10500198;
 RA Senaldi G., Varnum B.C., Sarmiento U., Starnes C., Lile J., Scully S.,
 RA Guo J., Elliott G., McNinch J., Shaklee C.L., Freeman D., Manu F.,
 RA Simonet W.S., Boone T., Chang M.-S.;
 RT "Novel neurotrophin-1/B cell-stimulating factor-3: a cytokine of the
 RT IL-6 family";
 RL Proc. Natl. Acad. Sci. U.S.A. 96:11458-11463(1999).
 DR EMBL; AF176913; AAF00993.1; -;
 DR MGD; MGI:1930086; Bsf3.
 DR GO; GO:0005125; P:cytokine activity; IDA.
 DR GO; GO:0030183; P:B-cell differentiation; IDA.
 DR GO; GO:0007166; P:cell surface receptor linked signal transdu...; IDA.
 DR GO; GO:0007259; P:JAK-STAT cascade; IDA.
 SQ SEQUENCE 225 AA; 25261 MW; 68B1FEAAB7F1A950 CRC64;
 Query Match 97.3%; Score 1193; DB 11; Length 225;
 Best Local Similarity 96.9%; Pred. No. 2e-104;
 Matches 218; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 1 MDRAGSWGMLACLTVMHLPALNRTGDPGPGSIQKTYDITRYLEHQLRSLAGT 60
 DB 1 MDRAGSWGMLACLTVMHLPALNRTGDPGPGSIQKTYDITRYLEHQLRSLAGT 60
 QY 61 YLNYLGPPFNEPDPNPRGLGAETLPRAATVLEWRSNDKRLTQNYEAYSHLLCYLRGL 120

DB 61 YLNYLGPPFNEPDPNPRGLGAETLPRAATVLEWRSNDKRLTQNYEAYSHLLCYLRGL 120
 QY 121 NRQAATAELRSLAHFCTSLQGLLSIAGVMAALGYPLPQPLPGTFTPTWPGFAHSDFLQ 180
 DB 121 NRQAATAELRSLAHFCTSLQGLLSIAGVMAALGYPLPQPLPGTFTPTWPGFAHSDFLQ 180
 QY 181 KMDDFWLLKELQWLRSAKDFNRLKKMQPPAAATVTLHGAHGF 225
 DB 181 KMDDFWLLKELQWLRSAKDFNRLKKMQPPAAATVTLHGAHGF 225
 RESULT 3
 QYQ2U1 PRELIMINARY; PRT; 215 AA.
 AC Q9PUJ1
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Receptivity factor isoform 2 precursor.
 GN PRF.
 OS Plethodon jordani (Jordan's salamander).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Caudata; Salamandroidea; Plethodontidae;
 OC Plethodon.
 OX NCBI_TaxID=8336;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=99420364; PubMed=10489368;
 RA Rollmann S.M., Houck L.D., Feldhoff R.C.;
 RT "Proteinaceous pheromone affecting female receptivity in a terrestrial
 RL Science 285:1907-1909(1999).
 DR EMBL; AF181481; AAF01026.1; -;
 KW Signal.
 FT SIGNAL
 SQ SEQUENCE 215 AA; 24080 MW; B341B8B7B4E28438 CRC64;
 Query Match 12.3%; Score 150.5; DB 13; Length 215;
 Best Local Similarity 26.2%; Pred. No. 4.1e-06;
 Matches 42; Conservative 31; Mismatches 80; Indels 7; Gaps 3;
 QY 56 SLACTYLYLGPPFNEPDPNPRGLGAETLPRAATVLEWRSNDKRLTQNYEAYSHLLC 115
 DB 55 SLLPTLYSLFQAGPLSDPDYQLPHIKVANLPTAAADYDTFMKQDTEKNNLIFYSAIVE 114
 QY 116 YLR-GLNRQ----AATAELRSLAHFCTSLQGLLSIAGVMAALGYPLPQPLPGTFTPT 170
 DB 115 FLKZANTEQEDLNPAELSLKAKFEAMANSNTLISKISDINTQMGMSVTITLP--KPLVV 172
 QY 171 PGPAAHDFLQKDDFWLLKELQWLRSAKDFNRLKKMQ 210
 DB 173 PFECSAYERKLRGVVCKEYKERVLLTKRDFEFLAKYQ 212
 RESULT 4
 QYQ2U0 PRELIMINARY; PRT; 215 AA.
 AC Q9PUJ0
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Receptivity factor isoform 3 precursor.
 GN PRF.
 OS Plethodon jordani (Jordan's salamander).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Caudata; Salamandroidea; Plethodontidae;
 OC Plethodon.
 OX NCBI_TaxID=8336;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=99420364; PubMed=10489368;
 RA Rollmann S.M., Houck L.D., Feldhoff R.C.;
 RT "Proteinaceous pheromone affecting female receptivity in a terrestrial


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Db      182  LEIRREGDPAALAEALAAATLPLMPC-----DISKAERYRLLDASSYSLS-- 228
QY      61  YNLYGPPNEPDPNPPRGAETLPRATVDLEWRSNDKRLTQNYEAYSH----- 112
Db      229  -----LPAPTNAETPLDDAYSALAWHLGSSORLASQYRPNHWRLLQDW 275
QY      113 -LILCYLRGLNRQAATAELRSLAHFCTSLQGLGSIAGVMAALGYPLPQPLPGTEPTWP 171
Db      276  EMLGELRALTSLSQGAAPTSTAQLETALDALLE-----WRFLVQ--AGQEDADVR 325
QY      172  GPAHSDFLOKMDPF-WLLKELQTLWRSKDF 202
Db      326  GAAHEQFLEELQDTRWGEFSLNTRWLLARSW 357

RESULT 8
Q96LS2  PRELIMINARY; PRT; 318 AA.
AC Q96LS2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein FLJ25132.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP TISSUE=Brain;
RC Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S.,
RA Fukuzumi Y., Fujimori Y., Komiyama M., Suzuki Y., Hata H.,
RA Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T.,
RA Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A., Kawakami B.,
RA Nagai K., Isegai T., Sugano S.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
KW Hypothetical protein.
SQ SEQUENCE 318 AA; 34305 MW; 625CFBLA599BF40 CRC64;

Query Match 8.0%; Score 97.5; DB 4; Length 318;
Best Local Similarity 25.1%; Pred. No. 0.68;
Matches 49; Conservative 19; Mismatches 76; Indels 51; Gaps 9;

QY 6 GDSWGMACIUCTVHLPAVPAALNRG---DPGPGFSIQTYDLYLEHQRLSLAGTYL 62
Db 82 GTECSFLIYLSEVWFQCPPLFERNQTAQAQAPKPPKQAVF-----RSNLSHL 131
QY 63 NYLGGPPNEPDPNPPRGAETL-----PRATVDLEW-----RSLNDKRLTQNYEAYS 111
Db 132 DLMGS-----GKSLFMKRTKLTQA---WALAAQLAQLGATORDQ--K 174
QY 112 HLLCYLRGLNRQAATAELRSLAHFCTSLQGLGSIAGVMA-----ALG-----YPLPOP 161
Db 175 QILVHIGFLFEESGDVFSPLVFLFCLSNALAWASALAPALATLTALGRALCRIPAPNP 234
QY 162 LPTGTEPTWTPGAHS 176
Db 235 LPSRSRTPSPPTVES 249

RESULT 9
Q8XOE9  PRELIMINARY; PRT; 530 AA.
AC Q8XOE9;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN B14A6.080.
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

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OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RA Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R.,
RA Nyakatura G., Mewes H.W., Mannhaupt G.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA German Neurospora genome project;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL670007; CAD21310.1;
DR InterPro; IPR001810; F-box.
DR PROSITE; PS50181; FBOX; 1.
KW Hypothetical protein.
SQ SEQUENCE 530 AA; 59352 MW; 70382EE15F71BB9D CRC64;

Query Match 8.0%; Score 97.5; DB 3; Length 530;
Best Local Similarity 24.8%; Pred. No. 1.3;
Matches 41; Conservative 22; Mismatches 65; Indels 37; Gaps 6;

QY 64 YLGPPNEPDPNPPRGAETLPRATVDLEWRSNDKRLTQNYEAYSHLLCYLRGLNR 122
Db 236 FLVPPYLEPDPFLVLAGLKKHLVDADLATHRDMEIQYLLFKKFLALTNLTWLR--- 291
QY 123 QAATAELRSLAHFCTSLQGLGSIAGVMAALGYPLPQPLPGT-----EPTWTPGP 173
Db 292 -----VNFERSISHY-----GKELLKWLASSLRPGTWSSPGLINADPSRLPPP 336
QY 174 AHSDFLOKMDPF-WLLKELQTLWRSKDFNRLKKKNQPPAAAVTL 218
Db 337 VEFDLQSLD----IGLDV----SANTLYRLENKFTSTLKATSL 373

RESULT 10
Q8GM87  PRELIMINARY; PRT; 8601 AA.
AC Q8GM87;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mixed type I polyketide synthase/nonribosomal peptide synthetase.
GN PEDF.
OS symbiont bacterium of Paederus fuscipes.
OC Bacteria.
OX NCBI_TaxID=176282;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22294974; PubMed=12381784;
RA Piel J.;
RT uncultured bacterial symbiont of Paederus beetles.;
RL Proc. Natl. Acad. Sci. U.S.A. 99:14002-14007(2002).
DR EMBL; AY059471; AAU27851.1;
DR GO; GO:0004024; F:alcohol dehydrogenase activity, zinc-dependent; IEA.
DR GO; GO:0004459; F:L-lactate dehydrogenase activity; IEA.
DR GO; GO:0016431; F:oxidoreductase activity; IEA.
DR GO; GO:0008757; F:S-adenosylmethionine-dependent methyltransf. .; IEA.
DR GO; GO:0005351; F:sugar porter activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.
DR GO; GO:0006036; P:glycolysis; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR GO; GO:0009401; P:phosphoenolpyruvate-dependent sugar phospho. .; IEA.
DR InterPro; IPR002198; ADH_short.
DR InterPro; IPR002328; ADH_zinc.
DR InterPro; IPR000873; AMP-bind.
DR InterPro; IPR001242; Condensatn.
DR InterPro; IPR002114; HPr_SerP_S.
DR InterPro; IPR000794; Ketoacyl_synth.
DR InterPro; IPR001557; L_LDH.
DR InterPro; IPR001601; Methyltransf.
DR InterPro; IPR006162; Ppantne_S.

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[illegible]

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RESULT 11
Q8NEV9
ID Q8NEV9 PRELIMINARY; PRT; 243 AA.
AC Q8NEV9;
DT 01-OCT-2002 (T-EMBLrel. 22, Created)
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE 11-27 p28 subunit.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
CX NCBI_TaxID=9606;
[1]
RN
RP SEQUENCE FROM N.A.
RA Pfanz S., Timans J., Cheung J., Rosales R., Kanzler H., Gilbert J.,
RA Habbert L., Churakova T., Travis M., Vaisberg E., Blumenschein W.,
RA Mattson J., Wagner J., To W., Zurawski S., McClanahan T., Gorman D.,
RA Bazan F., de Waal Malefyt R., Rennick D., Kastelein R.;
RT "11-27 p28 subunit sequences."
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY09296; AAK34498.1; -.
DR Genew; HGNC:19157; IL30.
DR GO; GO:0005615; C:extracellular space; ISS.
DR GO; GO:0045523; F:interleukin-27 receptor binding; ISS.
DR GO; GO:0005155; F:protein binding; ISS.
DR GO; GO:0005102; F:receptor binding; ISS.
DR GO; GO:0045078; P:positive regulation of interferon-gamma bio. .; IDA.
DR GO; GO:0042129; P:regulation of T-cell proliferation; ISS.
DR GO; GO:0045625; P:regulation of T-helper 1 cell differentiation; IDA.
SQ SEQUENCE 243 AA; 27476 MW; 2FA8A5E6CF61A98 CRC64;
Query Match 7.9%; Score 96.5; DB 4; Length 243;
Best Local Similarity 23.7%; Pred. No. 0.6;

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Matches 58; Conservative 26; Mismatches 104; Indels 57; Gaps 9;

Qy 1 MDLRAGD-SWGMACLCITVL-----WHLPAVPALNRTGDPGPGSIQK-----TYDL 46

Db 1.MGTAGDLGWLSILLPLLVQAGVWGFRPPG-----RQLSLQELRERFTVSUHL 53

Qy 47 TRYLEHQLRSLAGTYLN-----YLGPFNEPFDNPPRLGAEITLPRAIVDLEWRSLN 98

Db 54 ARKLLSEVRGQAHRAFAESHLFGVNLXLLP-----LG-EQLPDVSLTFQAMRRLS 101

Qy 99 DKRLRTQNEYAYSHLLCVLRGLNRQATAELRR-SLAHFTCTSLQGLLGSIAGVMAALGYP 157

Db 102 DPERLCISITLPPFHAPLGGLTGTQGWNTWERMQLWAMELDRLDQRHLRFQVLAAGFN 161

Qy 158 LPQP-----LPGETPTWTPGPAHSDFLOKMDDFWLLKELOTWLRSAKDF 202

Db 162 LPPEEEEEEEERKGLLPALGSAIQGPAQVSWPQLLSTVRLHLSLELVSRAVREL 221

Qy 203 NRLKK 207

Db 222 LLLSK 226

RESULT 12

Q8N358 PRELIMINARY; PRT; 287 AA.

AC Q8N358

DT 01-OCT-2002 (TREMBLrel. 22, Created)

DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)

DE 01-OCT-2002 (TREMBLrel. 22, Last annotation update)

DE Hypothetical protein.

OS Homo sapiens (Human).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_taxid=9606;

[1]

RN SEQUENCE FROM N.A.

RP TISSUE=Blood;

RC Strausberg R.;

RA Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC028076; AA028076.1; -.

KW Hypothetical protein.

SQ SEQUENCE 287 AA; 32156 MW; 65E71ECA0328E74E CRC64;

Query Match 7.7%; Score 94; DB 4; Length 287;

Best Local Similarity 22.3%; Pred. No. 1.3;

Matches 47; Conservative 18; Mismatches 62; Indels 84; Gaps 9;

Qy 15 LCTVLWHLPAVPALNRTGDPGPGSIQKTYD-----LTRY-----LSHQL--RSLAG 59

Db 132 LLPLVWLRP-----PDPGTLMILQCFSRQSPPGVLRFHNLQHLWVLTGRAFTN 181

Qy 60 TYLNY-----LGPFNEPFDNPPRLGAEITLPRAIVDLEWRSNDKRLRTQNEYAYSHLLC 115

Db 182 TYLFYGYRVRGP-----ESSVSYSRLA 204

Qy 116 YLRGLNRQATAELRRSLAHFTCTSLQGLLGSI-----GVMAALGYPLPQPLPGTEPTW 169

Db 205 YL-----LSPLACLILFCGTLHOLLTSLASGPGAGWPAPAHWPACPLPGLPRLQ 256

Qy 170 TPGPAHSDFLOKM-----DDFWLLKELOTWLM 196

Db 257 LPPPHHAQVLRAGAAGMGDTWRGRSFLPWGW 287

RESULT 13

Q8KNF2 PRELIMINARY; PRT; 392 AA.

AC Q8KNF2

DT 01-OCT-2002 (TREMBLrel. 22, Created)

DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)

DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)

DE Calg1.

GN CALGI.
 OS Micromonospora echinospora (Micromonospora purpurea).
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Micromonosporineae; Micromonosporaceae; Micromonospora.
 OX NCBI_TaxID=1877;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRRL 15839;
 RA Ahlert J., Shepard E., Lomovskaya N., Zazopoulos E., Staffa A.,
 RA Bachmann B.O., Huang K., Fonstein L., Czisny A., Whitam R.E.,
 RA Farnet C.M., Thorson J.S.;
 RT "The calicheamicin gene cluster and its iterative type I PKS.";
 RL Science 0:0-0(2002).
 DR EMBL: AF497482; C:intracellular; IEA.
 DR GO: GO:0005622; C:intracellular; IEA.
 DR GO: GO:0016301; P:kinase activity; IEA.
 DR GO: GO:0016774; P:phosphotransferase activity, carboxyl group. .; IEA.
 DR GO: GO:0016758; P:transferase activity, transferring hexosyl . .; IEA.
 DR GO: GO:0005975; P:carbohydrate metabolism; IEA.
 DR GO: GO:0030259; P:lipid glycosylation; IEA.
 DR GO: GO:0016310; P:phosphorylation; IEA.
 DR InterPro: IPR000890; Acetate kin.
 DR Pfam: PF03033; Glyco trans 28.
 DR PROSITE: PS01076; ACETATE_KINASE 2; 1.
 DR SEQUENCE 392 AA; 41151 MW; 8D298611281E065E CRC64;
 SQ
 Query Match 7.6%; Score 93; DB 2; Length 392;
 Best Local Similarity 26.4%; Pred. No. 2.4;
 Matches 43; Conservative 15; Mismatches 61; Indels 44; Gaps 7;
 QY 45 DLTRYLEHQLRSIA-----GTYLNYLGPFPNEPDF--NPPRLGAEITLPR 86
 DB 146 DLTRSEEEVGLAQRLGLDLPPGRIDGNGNPFIDIFPSLOEPEFRAPRHELRVPVF 205
 QY 87 ATV-DLEVVRSLNDKRLQNVAVSHLLCYLRGLNRQATAEALRRSLAHFCTSLQGLIG 145
 DB 206 AEQGDLPAMLSRDTR-----PLVYLTGTSSGGTVEVLRA-----AIDGLAG 249
 QY 146 SINGVAAALGYPLQPLQGTPE-----TWTGPA---HSDFL 179
 DB 250 LDADVLVAGPSLDVSGLGEVPAANVRLESWVQPAALLPHVDLV 292
 RESULT 14
 Q82G16 PRELIMINARY; PRT; 860 AA.
 AC Q82G16;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical protein.
 GN SAV3911.
 OS Streptomyces avermitilis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=33903;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
 RX MEDLINE=21477403; PubMed=11572948;
 RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
 RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osone T.,
 RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
 RT "Genome sequence of an industrial microorganism Streptomyces
 RT avermitilis: deducing the ability of producing secondary
 RT metabolites.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
 RX MEDLINE=22608306; PubMed=12692562;
 RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,

RA Sakaki Y., Hattori M., Omura S.;
 RT "Complete genome sequence and comparative analysis of the industrial
 RT microorganism Streptomyces avermitilis.";
 RL Nat. Biotechnol. 21:526-531(2003).
 DR EMBL: AP005037; BAC71623.1;
 RW Hypothetical protein; Complete proteome.
 S0 SEQUENCE 860 AA; 90116 MW; C7F0123F70226BC5 CRC64;
 Query Match 7.5%; Score 92.5; DB 16; Length 860;
 Best Local Similarity 27.2%; Pred. No. 7.3;
 Matches 56; Conservative 22; Mismatches 101; Indels 27; Gaps 9;
 QY 5 AGDSWGMALCLCTVL--WHLPAVPAALNRTGDPG-----PGPSIQKTYDLTRY 49
 DB 288 AGQAYTALATVEELLKDMH--EGGPAVLRAGGLSVRLKRTAVALDVPEPTAAFWVELT-Y 345
 QY 50 LEHQLRSLAGTYLNYLGPFPNEPDFNPPRLGAEITLPRATYDLEVRSLNDKRLQNTYEA 109
 DB 346 AAGLLASDGEAEERYAATPAYDEWLELP--AAERWSRLAT---AWLAATRTAGLVGRDA 400
 QY 110 YSHLLCYL-RGLNRQATAEALRRSLAHFCTSLQGLIGTAGYAAALGYPLQPLQGTPEPT 168
 DB 401 KERTLSALGFLGDRSAASEVRREVLLALLADLPEGASAPASVLARLRW--ERPLRGTHTPS 458
 QY 169 WTP--GPAHSDFLQKDDDFLLKELQ 192
 DB 459 PPSAPSSSSDDLRTRLAEWTLSEAE 484
 RESULT 15
 Q9MAU1 PRELIMINARY; PRT; 332 AA.
 AC Q9MAU1;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE F13M7.8 protein (Hypothetical protein).
 GN F13M7.8.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RA Vysotskaia V.S., Schwartz J.R., Toriumi M., Yu G., Kwan A., Liu, S.,
 RA Li J., Kremenetskaia I., Luros J., Araujo R., Au M., Bredel V.,
 RA Buehler E., Conway A., Dewar K., Feng J., Kim C., Kurtz D., Li Y.,
 RA Palm C., Shinn P., Sun H., Davis R., Becker J., Federspiel N.,
 RA Theologis A.;
 RT "The sequence of BAC F13M7 from Arabidopsis thaliana chromosome 1.";
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RA Theologis A.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov N.,
 RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
 RT "Full-length messenger RNA sequences greatly improve genome
 RT annotation.";
 RL Genome Biol. 0:0-0(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
 RA Feldmann K.;
 RT "Full-length cDNA from Arabidopsis thaliana.";
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC004809; AA740444.1;
 DR EMBL: AY085490; AAM62716.1;

DR PIR; G86182; G86182.
KW Hypothetical protein.
SQ SEQUENCE 332 AA; 36793 MW; 18E8697141A070F4 CRC64;
Query Match 7.5%; Score 92; DB 10; Length 332;
Best Local Similarity 26.4%; Pred. No. 2.4;
Matches 58; Conservative 24; Mismatches 72; Indels 66; Gaps 13;
QY 23 PAVPALNETGDPGPGPSQTKTYDLTRYLEHQLRSLAGTYLNY----- 64
Db 113 PSVTAGNLSGYF-PRPSF--TYDPGYEQRMESLLOQFIRERNPQIRPLRIGLGSFVG 169
QY 65 LGPPFNEPDPNPRLGAETLPRATVDLEWVWESLNDKLRLLTQNYEAYSHELLCYLGLNRQA 124
Db 170 LGPIRASPOFLQPRVAPP--PTSILD---TSRNRKAR-----SKDGLAVVVG--RKV 215
QY 125 ATAEIRSL-----AHFCTSLGGLGSIAGVMAALGYPLPOPPLP---GTEPTWT 170
Db 216 RITEGSSSLYSLGRSWLXNGAHV-----GIQPORSGIMK-----PLPKPLPVDLTTSVP 266
QY 171 PGPAHSDFLQKMDDFWLLKELQTLWLRSAKDFNRLKKMQ 210
Db 267 DDPDEESADEKDEEAVKQL-----SEKDL--LKRHIE 298

Search completed: August 10, 2004, 06:47:48
Job time : 38 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 10, 2004, 06:43:28 ; Search time 48 Seconds
(without alignments)
1324.441 Million cell updates/sec

Title: US-09-931-704-2

Perfect score: 1226

Sequence: 1 MDLRAGDSWGLACTVLM.....KKXMQPPAAATVHLGNKGF 225

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1226	100.0	225	2	AAW56141 Amino aci
2	1226	100.0	225	2	AAW29715 Human neu
3	1226	100.0	225	2	AAW94466 Human car
4	1226	100.0	225	3	AAW87813 Human NNT
5	1226	100.0	225	4	AAW63543 Amino aci
6	1226	100.0	225	5	AAU78176 Human nov
7	1226	100.0	253	4	AAW25831 Human pro
8	1214	99.0	223	4	AAE00828 Human car
9	1204	98.2	321	4	ABE11896 Human car
10	1204	98.2	321	4	AAW73399 Human pro
11	1197	97.6	260	4	AAW78415 Human pro
12	1193	97.3	225	2	AAW56142 Amino aci
13	1193	97.3	225	2	AAW29716 Mouse neu
14	1193	97.3	225	3	AAW87814 Murine NN
15	1193	97.3	225	5	AAU78177 Mouse nov
16	1169	95.4	215	3	AAW19586 Human int
17	1136	92.7	215	3	AAW19587 Mouse int
18	885	72.2	164	4	AAW20115 Peptide #
19	885	72.2	164	4	ABB40317 Peptide #
20	885	72.2	164	4	AAW34012 Peptide #
21	885	72.2	164	4	ABE24716 Protein #
22	885	72.2	164	4	AAW73827 Human bon
23	885	72.2	164	4	AAW61118 Human liv
24	885	72.2	164	4	ABG55577 Human liv
25	885	72.2	164	5	ABG43716 Human pep

AAy09197 Human DNA
AAy09196 Human DNA
AAr83965 Mouse car
AAr88204 Human car
AAw29237 Murine ca
Adc4999 Mouse CHF
Abu41629 Protein e
Aao29660 Paederus
AAu09153 Human cyt
Aab20277 Human int
ABg32291 Human IL-
AAu76375 Human hel
ABu09749 Human var
ABg75877 Human cyt
ABu12010 M. echino
Aag22132 Arabidops
Aag40321 Arabidops
AAr83967 Human car
AAw29238 Human car
AAy06490 Human tum

ALIGNMENTS

RESULT 1

AAW56141
ID AAW56141 standard; protein; 225 AA.

XX AAW56141;

XX AC (first entry)

DT 13-JUL-1998 (first entry)

DE Amino acid sequence of human neurotrophic factor NNT-1.
XX Human; neurotrophic factor; NNT-1; growth; motor; sympathetic; neuron;

KW treatment; neurological disease; degeneration; Parkinson's disease;
KW amyotrophic lateral sclerosis; ALS; Alzheimer's disease; stroke.
XX Homo sapiens.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..27

FT Protein /note= "signal peptide"

FT Protein 28..225

FT Protein /note= "mature protein"

FT Protein

FT Protein

FT Protein

FT Protein

FT Protein

FT Protein

FT Protein

FT Protein

FT Protein

FT Protein

FT Protein

FT Protein

FT Protein

FT Protein

FT Protein

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FT Protein

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FT Protein

FT Protein

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FT Protein

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FT Protein

FT Protein

FT Protein

FT Protein

FT Protein

FT Protein

CC and various degenerative disorders affecting vision

XX Sequence 225 AA;

Query Match 100.0%; Score 1226; DB 2; Length 225;

Best Local Similarity 100.0%; Pred. No. 4.8e-119; Mismatches 0; Indels 0; Gaps 0;

Matches 225; Conservative 0;

1 MDLRAGDSWGLACLTCTVWLHLPVAPALNRTGDPGPGSIQKTYDLYLHSHQLRSLAGT 60

1 MDLRAGDSWGLACLTCTVWLHLPVAPALNRTGDPGPGSIQKTYDLYLHSHQLRSLAGT 60

61 YLNYLGPPFNEPDPNPRGAEATLPRATVDLEVWRSNDKRLTONYAYSHLLCYLRGL 120

61 YLNYLGPPFNEPDPNPRGAEATLPRATVDLEVWRSNDKRLTONYAYSHLLCYLRGL 120

121 NRQAATAELRRSLAHFCTSLQGLLSIAGVMAALGYPLPQPLPGTEPTWTGPAHSDFLQ 180

121 NRQAATAELRRSLAHFCTSLQGLLSIAGVMAALGYPLPQPLPGTEPTWTGPAHSDFLQ 180

181 KYDDFWLLKELQTLWLRSAKDFNRLKKKQMPAAAVTLHLGAHGF 225

181 KYDDFWLLKELQTLWLRSAKDFNRLKKKQMPAAAVTLHLGAHGF 225

RESULT 2

AAW29715

ID AAW29715 standard; protein; 225 AA.

AC AAW29715;

DT 09-NOV-1998 (first entry)

XX Human neurotrophic factor NNT-1.

XX NNT-1; neurotrophic factor; human; antiinflammatory; adjuvant;
 KW Alzheimer's disease; Parkinson's disease; Huntington's disease;
 KW anyotrophic lateral sclerosis; Charcot-Marie-Tooth syndrome;
 KW peripheral neuropathy; dystrophy; neural retina degeneration;
 KW common variable immunodeficiency; CVID; selective IGA deficiency;
 KW hypogammaglobulinaemia; X-linked agammaglobulinaemia; antiseptic;
 KW therapy.

XX Homo sapiens.

XX Key Location/Qualifiers
 FT Peptide 1..27
 FT Protein /label= Sig_peptide
 FT /label= Mat_protein

XX WO9833922-A1.

XX 06-AUG-1998.

XX 02-FEB-1998; 98WO-US002363.

XX 03-FEB-1997; 97US-00792019.

XX 30-JAN-1998; 98US-00016534.

XX (AMGE-) AMGEN INC.

XX Chang M, Elliot GS, Senaldi G, Sarmiento U;

XX WPI; 1998-437475/37.

XX N-PSDB; AAV47510, AAV47511.

XX Newly isolated nucleic acid encoding human or murine neurotrophic factor
 NNT-1 - useful for treatment of neurological and immunological diseases
 or inflammation, also as vaccine adjuvant.

XX Claim 12; Fig 3; 120pp; English.

CC This is the amino acid sequence of a novel neurotrophic factor,
 CC designated NNT-1, that is a growth factor for neurons and for B or T
 CC cells. It was deduced from isolated cDNA (see AAV47510) and genomic DNA
 CC (see AAV47511) clones. Vectors containing the cDNA or genomic DNA and
 CC host cells are provided for use in the production of NNT-1 polypeptides.
 CC These are used to treat: (i) neurological or immunological diseases,
 CC specifically Alzheimer's, Parkinson's or Huntington's diseases, peripheral
 CC anyotrophic lateral sclerosis, Charcot-Marie-Tooth syndrome, the neural retina, or
 CC neuropathy, dystrophy and degeneration of the neural retina, or
 CC conditions characterised by T or B cell defects, e.g. common variable
 CC immunodeficiency (CVID), selective IGA deficiency, hypogammaglobulinaemia
 CC and X-linked agammaglobulinaemia (claimed), but many others disclosed;
 CC and (ii) inflammation. NNT-1 is also able to boost immunoreactivity and
 CC antibody production following vaccination, and, since it inhibits tumour
 CC necrosis factor production, it may also be useful for treating sepsis. In
 CC addition, cells that have been engineered to express NNT-1 can be
 CC implanted, or nucleic acids are delivered in gene therapy vectors

XX Sequence 225 AA;

Query Match 100.0%; Score 1226; DB 2; Length 225;

Best Local Similarity 100.0%; Pred. No. 4.8e-119;

Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLRAGDSWGLACLTCTVWLHLPVAPALNRTGDPGPGSIQKTYDLYLHSHQLRSLAGT 60

Db 1 MDLRAGDSWGLACLTCTVWLHLPVAPALNRTGDPGPGSIQKTYDLYLHSHQLRSLAGT 60

QY 61 YLNYLGPPFNEPDPNPRGAEATLPRATVDLEVWRSNDKRLTONYAYSHLLCYLRGL 120

Db 61 YLNYLGPPFNEPDPNPRGAEATLPRATVDLEVWRSNDKRLTONYAYSHLLCYLRGL 120

QY 121 NRQAATAELRRSLAHFCTSLQGLLSIAGVMAALGYPLPQPLPGTEPTWTGPAHSDFLQ 180

Db 121 NRQAATAELRRSLAHFCTSLQGLLSIAGVMAALGYPLPQPLPGTEPTWTGPAHSDFLQ 180

QY 181 KYDDFWLLKELQTLWLRSAKDFNRLKKKQMPAAAVTLHLGAHGF 225

Db 181 KYDDFWLLKELQTLWLRSAKDFNRLKKKQMPAAAVTLHLGAHGF 225

RESULT 3

AAW94466

ID AAW94466 standard; protein; 225 AA.

AC AAW94466;

DT 22-APR-1999 (first entry)

DE Human cardiotrophin-like cytokine protein.

XX Human; cardiotrophin-like cytokine; interleukin 6 cytokine family; C1C;
 KW IL-6; diagnosis; detection; immune system-related disorder; cancer;
 KW cardiac disorder; heart failure; hypertension; cancer;
 KW autoimmune disorder; infection.

XX Homo sapiens.

XX Key Location/Qualifiers
 FT Peptide 1..27
 FT Protein /label= signal
 FT /label= Cardiotrophin-like_cytokine
 FT Domain 28..225
 FT /label= CD-I
 FT /note= "conserved domain"
 FT Domain 74..79
 FT /label= CD-II
 FT /note= "conserved domain"
 FT Domain 150..156
 FT /label= CD-III
 FT /note= "conserved domain"

```

PN WO9900415-A1.
XX
XX 07-JAN-1999.
XX
XX 29-JUN-1998; 98WO-US013129.
XX
XX 30-JUN-1997; 97US-0051311P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Shi Y, Ruben SM;
XX
XX WPI; 1999-095678/08.
XX
XX N-PSDB; AAX16161.
XX
XX New isolated cardiostrophin-like cytokine nucleic acid - used to develop
XX products for treating cardiac and immune system disorders, e.g. heart
XX failure, hypertension, cancers, autoimmune disorders and infections.
XX
XX Claim 1; Fig 1; 103pp; English.
XX
XX The present invention relates to a novel cardiostrophin-like cytokine
XX (CLC) protein which is a member of the interleukin 6 (IL-6) cytokine
XX family. The present sequence represents the human CLC protein. The
XX present invention also describes screening methods for identifying
XX agonists and antagonists of CLC activity, as well as methods for
XX detecting cardiac and immune system-related disorders and therapeutic
XX methods for treating cardiac and immune system-related disorders, e.g
XX heart failure, hypertension, cancers, autoimmune disorders and infections
XX
XX Sequence 225 AA;
XX
XX Query Match 100.0%; Score 1226; DB 2; Length 225;
XX Best Local Similarity 100.0%; Pred. No. 4.8e-119;
XX Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 MDLRAGDSWGMCLCTVWLHLPVAPALNRTGDPGPGPSIQKTYDLTRYLHQLRSLAGT 60
XX DB 1 MDLRAGDSWGMCLCTVWLHLPVAPALNRTGDPGPGPSIQKTYDLTRYLHQLRSLAGT 60
XX
XX QY 61 YLNYLGPPFPNEPDPNPPRLGAEATLPRATVDLEVWRSNDKRLTQNYEAYSHLLCYLRGL 120
XX DB 61 YLNYLGPPFPNEPDPNPPRLGAEATLPRATVDLEVWRSNDKRLTQNYEAYSHLLCYLRGL 120
XX
XX QY 121 NRQAATAELRSLAHFCTSLQGLLSIAGVMAALGYPLPQPLPGTPTWTTPGPAHSDFLQ 180
XX DB 121 NRQAATAELRSLAHFCTSLQGLLSIAGVMAALGYPLPQPLPGTPTWTTPGPAHSDFLQ 180
XX
XX QY 181 KMDDFWLLKELQTLWRSKADFNRLKKMKQPPAAAVTLHLGAHGF 225
XX DB 181 KMDDFWLLKELQTLWRSKADFNRLKKMKQPPAAAVTLHLGAHGF 225
XX
XX RESULT 4
XX ID AAY87813 standard; protein; 225 AA.
XX
XX AC AAY87813;
XX
XX XX 24-AUG-2000 (first entry)
XX
XX DE Human NNT-1 protein.
XX
XX NNT-1; human; neurotrophic factor; neurotrophic; neuroprotective; treatment;
XX anticonvulsant; antiparkinsonian; antidiabetic; ophthalmological;
XX nervous system degeneration; Alzheimer's disease; Parkinson's disease;
XX amyotrophic lateral sclerosis; Charcot-Marie-Tooth syndrome;
XX Huntington's disease; peripheral neuropathy; neural retina degeneration;
XX retinopathy; immune disorder; hematopoietic disorder.
XX
XX Homo sapiens.
XX
XX OS
XX XX
XX PN US6054294-A.

```

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XX 25-APR-2000.
XX
XX 12-DEC-1997; 97US-00988819.
XX
XX 03-FEB-1997; 97US-00792019.
XX
XX (AMGE-) AMGEN INC.
XX
XX Chang M;
XX
XX WPI; 2000-338492/29.
XX
XX N-PSDB; AAA39481.
XX
XX New nucleic acids encoding neurotrophic factors useful for stimulating
XX growth of motor or sympathetic neurons for treating neuron cell damage.
XX
XX Claim 1c; Fig 3; 42pp; English.
XX
XX This invention describes a novel nucleic acid molecule (I) encoding a
XX novel neurotrophic factor (NNT-1) (II) which has neurotrophic,
XX neuroprotective, anticonvulsant, antiparkinsonian, antidiabetic and
XX ophthalmological activity. (I) is useful for producing NNT-1 polypeptides
XX which are useful for treating patients in whom various cells of the
XX central, autonomic, or peripheral nervous system have degenerated and/or
XX have been damaged by congenital disease, trauma, mechanical damage,
XX surgery, stroke, ischemia, infection, metabolic disease, nutritional
XX deficiency, malignancy and/or toxic agents. NNT-1 proteins are used to
XX treat diseases like Alzheimer's, Parkinson's, amyotrophic lateral
XX sclerosis, Charcot-Marie-Tooth syndrome, Huntington's disease, peripheral
XX neuropathy induced by diabetes or other metabolic disorders, and/or
XX dystrophies or degeneration of the neural retina such as retinitis
XX pigmentosa, drug-induced retinopathies, stationary forms of night
XX blindness, progressive cone-rod degeneration, immune disorders and
XX hematopoietic disorders. (I) is effective in treating neurological
XX conditions and promotes neuron regeneration. Neural functions are
XX effectively restored in patients suffering from various neurological
XX disorders. This sequence represents the human NNT-1 protein described in
XX the method of the invention
XX
XX Sequence 225 AA;
XX
XX Query Match 100.0%; Score 1226; DB 3; Length 225;
XX Best Local Similarity 100.0%; Pred. No. 4.8e-119;
XX Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 MDLRAGDSWGMCLCTVWLHLPVAPALNRTGDPGPGPSIQKTYDLTRYLHQLRSLAGT 60
XX DB 1 MDLRAGDSWGMCLCTVWLHLPVAPALNRTGDPGPGPSIQKTYDLTRYLHQLRSLAGT 60
XX
XX QY 61 YLNYLGPPFPNEPDPNPPRLGAEATLPRATVDLEVWRSNDKRLTQNYEAYSHLLCYLRGL 120
XX DB 61 YLNYLGPPFPNEPDPNPPRLGAEATLPRATVDLEVWRSNDKRLTQNYEAYSHLLCYLRGL 120
XX
XX QY 121 NRQAATAELRSLAHFCTSLQGLLSIAGVMAALGYPLPQPLPGTPTWTTPGPAHSDFLQ 180
XX DB 121 NRQAATAELRSLAHFCTSLQGLLSIAGVMAALGYPLPQPLPGTPTWTTPGPAHSDFLQ 180
XX
XX QY 181 KMDDFWLLKELQTLWRSKADFNRLKKMKQPPAAAVTLHLGAHGF 225
XX DB 181 KMDDFWLLKELQTLWRSKADFNRLKKMKQPPAAAVTLHLGAHGF 225
XX
XX RESULT 5
XX AAG63543
XX ID AAG63543 standard; protein; 225 AA.
XX
XX AC AAG63543;
XX
XX XX 15-OCT-2001 (first entry)
XX
XX DE Amino acid sequence of a human NNT-1 protein.
XX
XX

```

NNT-1; CLF-1; SCNTFralpha; nervous system; neuron; nervous system; neuro-muscular function; tumour; immune system; haematopoietic disease; reproductive system; liver; skeletal muscle; neurodegenerative disease; amyotrophic lateral sclerosis; Parkinson's disease; Huntington's disease; muscular mass; paralysis; cancer; obesity; fertility; endometriosis; blastocyst implantation; thrombosis; retinal disease; retinal pigmentosis.

XX Homo sapiens.

OS WC2001551172-A2.

XX 02-AUG-2001.

XX 26-JAN-2001; 2001WO-FR000253.

XX 27-JAN-2000; 2000FR-00001035.

XX 12-OCT-2000; 2000FR-00013089.

XX (FABR) FABRE MEDICAMENT SA PIERRE.

PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.

XX Elson G, Gauchat J, Plun-Favreau H, Chevalier S, Gascan H;

PI WPI; 2001-488773/53.

DR N-PSDB; AAH74484.

DR A complex comprising a NNT-1 protein and a CLF-1 and/or SCNTFralpha protein useful to treat neurodegenerative disease including Parkinson's disease and Huntington's, obesity and cancer.

XX Claim 2; Page 58; 67pp; French.

XX The present sequence represents a human NNT-1 protein. The specification describes a complex comprising a NNT-1 protein and a CLF-1 and/or SCNTFralpha protein. The NNT-1/CLF-1 complex is used to modulate activity of the SCNTFralpha/gp130/LiFrbeta receptor complex, or to induce phosphorylation of the tyrosine of gp130 and LiFrbeta, particularly where cells expressing the receptor complex are in the central or peripheral nervous system, in neurons implicated in neuro-muscular function or in skeletal muscle. The complex or antibodies are also used to decrease the survival, growth or proliferation of tumour cells or to facilitate the proliferation and/or inhibit differentiation of cells stocks. The complex is also used to modulate activity of the gp130/LiFrbeta receptor or cells expressing that receptor, particularly those cells implicated in the immune, haematopoietic, nervous or reproductive system, the liver or skeletal muscle. Molecules of the invention may be used to prevent or treat neurodegenerative diseases including amyotrophic lateral sclerosis, Parkinson's and Huntington's disease, to repair or regenerate nervous or muscular tissue or to maintain muscular mass in paralytic patients. They may also be used to treat cancer, obesity and associated diseases, and to improve fertility, particularly to avoid endometriosis and/or assist blastocyst implantation, thrombosis, or retinal disease, particular retinal pigmentosis

XX Sequence 225 AA;

XX Query Match 100.0%; Score 1226; DB 4; Length 225;

XX Best Local Similarity 100.0%; Pred. No. 4,8e-119;

XX Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 MDLRAGDSGMLACLTIVLWHPVAPALNRTGDPGPGPSIOKTVDLTRYLEHQIRSLAGT 60

DB 1 MDLRAGDSGMLACLTIVLWHPVAPALNRTGDPGPGPSIOKTVDLTRYLEHQIRSLAGT 60

QY 61 YLNYLGPPNEPDNPPRLGASTLPRA TVDLEWRSNDKRLTQNYEAYSHLLCYLRGL 120

DB 61 YLNYLGPPNEPDNPPRLGASTLPRA TVDLEWRSNDKRLTQNYEAYSHLLCYLRGL 120

QY 121 NRCQATAELRRSLAHFCTSLQGLGSIAGVWAAALGYLPQLPGTEPTWTPGAHSDFLQ 180

DB 121 NRCQATAELRRSLAHFCTSLQGLGSIAGVWAAALGYLPQLPGTEPTWTPGAHSDFLQ 180

181 KWDDEFLLKELQTLWRSKDFNRLKKMKQPPAAAAVTLHLGAHGF 225
181 KWDDEFLLKELQTLWRSKDFNRLKKMKQPPAAAAVTLHLGAHGF 225

Db

RESULT 6
AAU78176
ID AAU78176 standard; protein; 225 AA.
XX
AC AAU78176;
XX
DT 05-JUN-2002 (first entry)
XX
DE Human novel neurotrophic factor NNT1.
XX
KW Human; NNT1; neurotrophic factor; IgE-related disease;
KW Type I allergic disease; allergic rhinitis; eczema; dermatitis;
KW pollinosis; asthma; immune disease; cancer; arteriosclerosis;
KW vascular restenosis; rheumatoid arthritis; psoriatic arthritis;
KW inflammatory arthritis; osteoarthritis; inflammatory joint disease;
KW autoimmune disease; multiple sclerosis; lupus; diabetes; endometriosis;
KW inflammatory bowel disease; transplant rejection; reproductive disorder;
KW graft versus host disease; infertility; miscarriage; preterm labour.
XX
XX Homo sapiens.
XX
OS W0200215977-A2.
PN
XX
PD 28-FEB-2002.
PP
PF 17-AUG-2001; 2001WO-US025906.
XX
PR 18-AUG-2001; 2000US-0226436P.
PR 16-AUG-2001; 2001US-00931704.
XX
XX (AMGE-) AMGEN INC.
PA
XX
XX Senaldi G;
PI
XX
XX WPI: 2002-280867/32.
DR N-PSDB; ABK11647.
XX
XX
XX Treating Immunoglobulin E-related disease, modulating IgE levels in a patient, preventing IgE-related disease and treating allergic diseases, involves administering NNT-1 inhibitor to a patient.
XX
XX
XX Claim 2; Fig 3; 63pp; English.
XX
XX The invention relates to treating Immunoglobulin E (IgE)-related disease, modulating IgE levels in a patient, preventing an IgE-related disease, and treating allergic diseases, comprising administering a therapeutically effective amount of novel neurotrophic factor (NNT)-1 inhibitor to a patient. Also included are a method of diagnosing an IgE-related disease or susceptibility to an IgE-related disease, by determining the presence or amount of expression of an NNT1 polypeptide encoded by a NNT1 nucleotide sequence, its fragment or naturally occurring variant, and diagnosing an IgE-related disease or susceptibility of an IgE-related disease based on the presence or amount of expression of the polypeptide and a pharmaceutical composition for use in treating IgE-related disease, comprising the NNT1 inhibitor. The NNT1 inhibitor is useful for preventing and treating IgE-related disease, modulating IgE levels, and treating allergic diseases e.g. Type I allergic disease, allergic rhinitis, eczema, dermatitis, pollinosis, asthma, immune diseases and disorders, diseases involving abnormal cell proliferation including cancer, arteriosclerosis and vascular restenosis, diseases and conditions relating to dysfunction of immune system including rheumatoid arthritis, psoriatic arthritis, inflammatory arthritis, osteoarthritis, inflammatory joint disease, autoimmune disease, multiple sclerosis, lupus, diabetes, inflammatory bowel disease, transplant rejection, and graft versus host disease, and reproductive diseases and disorders including infertility, miscarriage, preterm labour and delivery, and endometriosis. The present sequence represents human NNT1


```

XX  Sequence 225 AA;
SQ
  Query Match      100.0%; Score 1226; DB 5; Length 225;
  Best Local Similarity 100.0%; Pred. No. 4.8e-119;
  Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 MDLRAGDSWGLACLTVLWHLPAVPALNRTGDPGPGSIQKTYDLTRYLEHQURSLAGT 60
DQ  1 MDLRAGDSWGLACLTVLWHLPAVPALNRTGDPGPGSIQKTYDLTRYLEHQURSLAGT 60

QY  61 YLNYLGPPFPNEPDPNPPRLGAETLPRAVDLEWRSNDKRLTONYEAYSHLLCYLRGL 120
DQ  61 YLNYLGPPFPNEPDPNPPRLGAETLPRAVDLEWRSNDKRLTONYEAYSHLLCYLRGL 120

QY  121 NRQATAELRSLAHFCTSLQGLGSIAGVMAALGYPLPQLPQTEPTWTPGPAHSDFLQ 180
DQ  121 NRQATAELRSLAHFCTSLQGLGSIAGVMAALGYPLPQLPQTEPTWTPGPAHSDFLQ 180

QY  181 KMDDFWLLKELQTLWRSKDFNRLKKKQKQPPAAAVTLHLGAHGF 225
DQ  181 KMDDFWLLKELQTLWRSKDFNRLKKKQKQPPAAAVTLHLGAHGF 225

RESULT 7
AAM25831
ID  AAM25831 standard; protein; 253 AA.
AC  AAM25831;
DT  16-OCT-2001 (first entry)
DE  Human protein sequence SEQ ID NO:1346.
KW  Human; cancer; ulcer; HIV infection; human immunodeficiency virus;
KW  antiinflammatory; antirheumatic; antiarthritic; immunosuppressive;
KW  antibacterial; endocrine; cardiant; central nervous system; virucide;
KW  anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia;
KW  antiagregant; haemostatic; vulnary; antiulcer; osteopathic; eczema;
KW  dermatological; anti-allergic; antiasthmatic; antidiabetic; cytostatic;
KW  neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;
KW  immunostimulant; gene therapy; antitense therapy; vaccine; inflammation;
KW  antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;
KW  cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;
KW  genetic disease; haematopoietic disorder; platelet disorder; asthma;
KW  thrombocytopaenia; severe combined immunodeficiency;
KW  allergic rhinitis; diabetes; multiple sclerosis; depression;
KW  Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
KW  neurological disorder.
OS  Homo sapiens.
XX
XX  WO200153455-A2.
XX
XX  26-JUL-2001.
XX
XX  22-DEC-2000; 2000WO-US035017.
XX
XX  23-DEC-1999; 99US-00471275.
XX
XX  21-JAN-2000; 2000US-00488725.
XX
XX  25-APR-2000; 2000US-00552317.
XX
XX  (HYSE-) HYSEQ INC.
XX
XX  Tang YT, Liu C, Drmanac RT;
XX
XX  WPI; 2001-457603/49.
XX
XX  N-PSDB; AAH99772.
XX
XX  Isolated human polynucleotides encoding polypeptides, useful for the
XX  treatment and diagnosis of e.g. cancer, ulcers and HIV infection.
XX
XX  Claim 20; Page 278; 1217pp; English.
PS

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XX  AAH99166 to AAH99904 encode the human proteins given in AAM25225 to
XX  AAM25963. The proteins can have activities based on the tissues and cells
XX  they are expressed in, such as: antiinflammatory; antirheumatic;
XX  antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant;
XX  central nervous system; virucide; anti-HIV; fungicide; antimutagen;
XX  cardiovascular; antianaemic; antiagregant; haemostatic; vulnary;
XX  antiulcer; osteopathic; dermatological; anti-allergic; antiasthmatic;
XX  antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic;
XX  antiparkinsonian; and immunostimulant. The proteins and polynucleotides
XX  encoding them can be used in gene therapy, antitense therapy and vaccine
XX  production. The proteins and polynucleotides are useful for screening for
XX  agonists or antagonists of a protein and for the treatment and diagnosis
XX  of disorders associated with the activity of a protein e.g. inflammation,
XX  rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,
XX  neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal
XX  infections, autoimmunity, genetic diseases, haematopoietic disorders,
XX  anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers,
XX  osteoporosis, severe combined immunodeficiency, eczema, allergic
XX  rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,
XX  Alzheimer's disease, Parkinson's disease, neurodegenerative and
XX  neurological disorders
XX
SQ  Sequence 253 AA;
  Query Match      100.0%; Score 1226; DB 4; Length 253;
  Best Local Similarity 100.0%; Pred. No. 5.6e-119;
  Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 MDLRAGDSWGLACLTVLWHLPAVPALNRTGDPGPGSIQKTYDLTRYLEHQURSLAGT 60
DQ  29 MDLRAGDSWGLACLTVLWHLPAVPALNRTGDPGPGSIQKTYDLTRYLEHQURSLAGT 88

QY  61 YLNYLGPPFPNEPDPNPPRLGAETLPRAVDLEWRSNDKRLTONYEAYSHLLCYLRGL 120
DQ  89 YLNYLGPPFPNEPDPNPPRLGAETLPRAVDLEWRSNDKRLTONYEAYSHLLCYLRGL 148

QY  121 NRQATAELRSLAHFCTSLQGLGSIAGVMAALGYPLPQLPQTEPTWTPGPAHSDFLQ 180
DQ  149 NRQATAELRSLAHFCTSLQGLGSIAGVMAALGYPLPQLPQTEPTWTPGPAHSDFLQ 208

QY  181 KMDDFWLLKELQTLWRSKDFNRLKKKQKQPPAAAVTLHLGAHGF 225
DQ  209 KMDDFWLLKELQTLWRSKDFNRLKKKQKQPPAAAVTLHLGAHGF 253

RESULT 8
AAE00828
ID  AAE00828 standard; protein; 223 AA.
XX
XX  AAE00828;
XX
XX  02-JUL-2001 (first entry)
XX
XX  Human cardiotrophin-like cytokine (CLC) protein.
XX
XX  Human; biologically active complex; haemopoietin receptor; NR6;
XX  cardiotrophin-like cytokine; CLC; therapy; prophylaxis; proliferation;
XX  differentiation; cell survival; neurotrophic activity.
XX
XX  Homo sapiens.
XX
XX  Key      Location/Qualifiers
XX  Peptide  1..27
XX          /label= Signal_peptide
XX  Protein  28..223
XX          /label= Human_mature_CLC_protein
XX          /note= "Cardiotrophin-like cytokine"
XX
XX  WO200127157-A1.
XX
XX  19-APR-2001.
XX

```

PF 06-OCT-2000; 2000WO-AU001216.
 XX 08-OCT-1999; 99AU-00003327.
 PR 12-MAY-2000; 2000AU-00007489.
 XX (AMRA-) AMRAD OPERATIONS PTY LTD.
 XX Nash A, Jachno KM, Fabri LJ, Reid K, Bartlett PF, Hilton DJ;
 PI Nakata Y, Hasegawa M;
 XX WPI; 2001-281978/29.
 DR N-PSDB; AAD04201.
 XX New biologically active complex comprising NR6 and cardiotrophin-like-
 PT cytokine, for facilitating proliferation, differentiation and/or survival
 PT of a cell.
 XX Claim 32; Page 114-115; 123pp; English.
 XX The present invention relates to a biologically active complex comprising
 CC a haemopoietin receptor, NR6 and cardiotrophin-like cytokine (CLC). The
 CC complex is useful in the manufacture of a medicament for the treatment
 CC and/or prophylaxis of a subject, as it is involved in facilitating
 CC proliferation, differentiation and/or survival of a cell. The complex or
 CC its components have neurotrophic activity. The present sequence is human
 CC cardiotrophin-like cytokine (CLC) protein
 XX Sequence 223 AA;
 SQ
 Query Match 99.0%; Score 1214; DB 4; Length 223;
 Best Local Similarity 100.0%; Pred. No. 8.4e-118; Indels 0; Gaps 0;
 Matches 223; Conservative 0; Mismatches 0;
 QY 1 MDLRAGDSWGMCLACTVLWHLPAVPAALNRGTGDPGPGSIQKTYDLTRYLEHQLSLAGT 60
 DB 1 MDLRAGDSWGMCLACTVLWHLPAVPAALNRGTGDPGPGSIQKTYDLTRYLEHQLSLAGT 60
 QY 61 YLNYLGPPNPPNPPRIGAEPLPRATVDLEWRSNDKRLTQNYEAYSHLLCYLRLGL 120
 DB 61 YLNYLGPPNPPNPPRIGAEPLPRATVDLEWRSNDKRLTQNYEAYSHLLCYLRLGL 120
 QY 121 NQAQTAELRSLRAHFTCSLQGLGSIAGVMAALGYPLPQPLPGTEPTWTPGAHSDFLQ 180
 DB 121 NQAQTAELRSLRAHFTCSLQGLGSIAGVMAALGYPLPQPLPGTEPTWTPGAHSDFLQ 180
 QY 181 KMDDFWLLKELQWLRSAKDFNRLKKKQPPAAATVHLGAH 223
 DB 181 KMDDFWLLKELQWLRSAKDFNRLKKKQPPAAATVHLGAH 223
 RESULT 9
 ABB11896
 ID ABB11896 standard; peptide; 321 AA.
 XX ABB11896;
 AC
 XX 11-JAN-2002 (first entry)
 DT
 XX Human cardiotrophin-like cytokine homologue, SEQ ID NO:2266.
 DE
 XX Human; cytokine; cell proliferation; cell differentiation; growth factor;
 XX haematopoiesis regulation; tissue growth; immunomodulator; activin;
 KW inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
 KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
 KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
 KW chronic inflammatory condition; proliferative retinopathy;
 KW atherosclerosis; coronary heart disease; arterial ischaemia;
 KW bone disorder; osteoporosis; vascular growth disorder;
 KW tissue regeneration; wound healing; infection; immune disorder;
 KW cell culture; drug screening; gene therapy; antiinflammatory;
 KW antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
 KW cytosstatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
 KW antifungal; vulnery; antiulcer.

XX Homo sapiens.
 OS
 XX WO200157188-A2.
 PN
 XX 09-AUG-2001.
 PD
 XX 05-FEB-2001; 2001WO-US003800.
 PF
 XX 03-FEB-2000; 2000US-00496914.
 PR
 XX 27-APR-2000; 2000US-00560875.
 XX (HYSE-) HYSEQ INC.
 PA
 XX Tang YT, Liu C, Drmanac RT;
 PI WPI; 2001-457740/49.
 XX N-PSDB; ABA09140.
 DR
 XX Human proteins and DNA encoding sequences useful for preventing, treating
 PT or ameliorating a medical condition in a mammalian subject e.g. arthritis
 PT and cancer.
 XX Claim 20; Page 273; 1963pp; English.
 XX Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
 CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
 CC invention also relates to vectors and recombinant host cells comprising a
 CC nucleotide of the invention, methods of producing the novel polypeptides,
 CC antibodies against the polypeptides, methods of detecting the nucleotides
 CC or polypeptides in a sample, and methods of identifying compounds which
 CC bind to polypeptides of the invention. Although novel, many of the
 CC polypeptides of the invention have homology to known proteins, and hence
 CC giving an insight into their probable biological activities, and hence
 CC potential therapeutic applications. The polypeptides of the invention may
 CC have various activities, including cytokine, cell proliferation or cell
 CC differentiation activities; stem cell growth factor activity;
 CC haematopoiesis regulatory activity; tissue growth activity;
 CC immunomodulatory activity; activin- or inhibin-related activities;
 CC chemotactic or chemokinetic activities; haemostatic, thrombotic or
 CC thrombolytic activities; receptor or ligand activities; or may be
 CC involved in oncogenesis, cancer cell proliferation or metastasis.
 CC Depending on their biological activities, polypeptides and nucleotides of
 CC the invention are useful for preventing, treating or ameliorating medical
 CC conditions, e.g., by protein or gene therapy. Such conditions include
 CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell
 CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
 CC proliferative retinopathy, atherosclerosis, coronary heart disease,
 CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
 CC vascular growth. Polypeptides involved with tissue regeneration and
 CC repair (or nucleic acids encoding them) may be used to promote wound
 CC healing (e.g., of burns, incisions and ulcers), while those with
 CC immunomodulatory activities may be used in the treatment of viral,
 CC bacterial and fungal infections in addition to immune disorders.
 CC Polypeptides with growth factor activity may be used in cell cultures to
 CC promote cell growth. For example, such polypeptides may be used to
 CC manipulate stem cells in culture to give rise to neuroepithelial cells
 CC that can be used to augment or replace cells damaged by illness, the
 CC autoimmune disease or accidental damage. The polypeptides and nucleotides
 CC may also be used in the diagnosis of the above conditions, and in drug
 CC screening techniques. The present sequence represents a novel human
 CC polypeptide of the invention
 XX Sequence 321 AA;
 SQ
 Query Match 98.2%; Score 1204; DB 4; Length 321;
 Best Local Similarity 99.1%; Pred. No. 1.5e-116;
 Matches 221; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 3 LRAGDSWGMCLACTVLWHLPAVPAALNRGTGDPGPGSIQKTYDLTRYLEHQLSLAGT 62
 DB 99 LPTGDSWGMCLACTVLWHLPAVPAALNRGTGDPGPGSIQKTYDLTRYLEHQLSLAGT 158

QY 63 NYLGGPPNEPDNPPRLGAETLPRATVDLEWRSNDKRLRLTONYEAYSHLLCYLRGLNR 122
 Db 159 NYLGGPPNEPDNPPRLGAETLPRATVDLEWRSNDKRLRLTONYEAYSHLLCYLRGLNR 218
 QY 123 QAATAELRRSLAHFCTSLQGLLGSAGVMAALGYPLPQPLPGTEPTWTPGPAHSDFLQKM 182
 Db 219 QAATAELRRSLAHFCTSLQGLLGSAGVMAALGYPLPQPLPGTEPTWTPGPAHSDFLQKM 278
 QY 183 DDFWLLKELQTLWRSKDFNRLKKMKQPPAAAVTLHLGAHGF 225
 Db 279 DDFWLLKELQTLWRSKDFNRLKKMKQPPAAAVTLHLGAHGF 321

RESULT 10

AAAM79399
 ID AAM79399 standard; protein; 321 AA.

XX AC AAM79399;

XX DT 06-NOV-2001 (first entry)

XX DE Human protein SEQ ID NO 3045.

XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorder; arthritis; inflammation.

XX OS Homo sapiens.

XX PN WO200157190-A2.

XX PD 09-AUG-2001.

XX PF 05-FEB-2001; 2001WO-US004098.

XX PR 03-FEB-2000; 2000US-00496914.

XX PR 27-APR-2000; 2000US-00560875.

XX PR 20-JUN-2000; 2000US-00598075.

XX PR 19-JUL-2000; 2000US-00620325.

XX PR 01-SEP-2000; 2000US-00654936.

XX PR 15-SEP-2000; 2000US-00663561.

XX PR 20-OCT-2000; 2000US-00693325.

XX PR 30-NOV-2000; 2000US-00728422.

XX PA (HYSE-) HYSEQ INC.

XX PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;

XX PI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;

XX PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;

XX PR WPI; 2001-476283/51.

XX DR N-PSDB; AAK52532.

XX Nucleic acids encoding polypeptides with cytokine-like activities, useful

XX in diagnosis and gene therapy.

XX Claim 20; Page 237; 6221pp; English.

XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
 CC encoded polypeptides (AAM78323-AAK80302) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
 CC (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
 CC sequence listing were missing at the time of publication

SQ Sequence 321 AA;

Query Match 98.2%; Score 1204; DB 4; Length 321;

Best Local Similarity 99.1%; Pred. No. 1.5e-116;

Matches 221; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 LRAGDSWGMCLACTVWLHPAPVAPALNRTGDPGPGPSIOKTYDLTRYLEHQLRSLAGTYL 62

Db 99 LFTGDSWGMCLACTVWLHPAPVAPALNRTGDPGPGPSIOKTYDLTRYLEHQLRSLAGTYL 158

QY 63 NYLGGPPNEPDNPPRLGAETLPRATVDLEWRSNDKRLRLTONYEAYSHLLCYLRGLNR 122

Db 159 NYLGGPPNEPDNPPRLGAETLPRATVDLEWRSNDKRLRLTONYEAYSHLLCYLRGLNR 218

QY 123 QAATAELRRSLAHFCTSLQGLLGSAGVMAALGYPLPQPLPGTEPTWTPGPAHSDFLQKM 182

Db 219 QAATAELRRSLAHFCTSLQGLLGSAGVMAALGYPLPQPLPGTEPTWTPGPAHSDFLQKM 278

QY 183 DDFWLLKELQTLWRSKDFNRLKKMKQPPAAAVTLHLGAHGF 225

Db 279 DDFWLLKELQTLWRSKDFNRLKKMKQPPAAAVTLHLGAHGF 321

RESULT 11

AAAM78415

ID AAM78415 standard; protein; 260 AA.

XX AC AAM78415;

XX DT 06-NOV-2001 (first entry)

XX DE Human protein SEQ ID NO 1077.

XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;

KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;

KW tissue growth factor; immunomodulatory; cancer; leukaemia;

KW nervous system disorder; arthritis; inflammation.

XX OS Homo sapiens.

XX PN WO200157190-A2.

XX PD 09-AUG-2001.

XX PF 05-FEB-2001; 2001WO-US004098.

XX PR 03-FEB-2000; 2000US-00496914.

XX PR 27-APR-2000; 2000US-00560875.

XX PR 20-JUN-2000; 2000US-00598075.

XX PR 19-JUL-2000; 2000US-00620325.

XX PR 01-SEP-2000; 2000US-00654936.

XX PR 15-SEP-2000; 2000US-00663561.

XX PR 20-OCT-2000; 2000US-00693325.

XX PR 30-NOV-2000; 2000US-00728422.

XX PA (HYSE-) HYSEQ INC.

XX PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;

XX PI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;

XX PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;

XX PR WPI; 2001-476283/51.

XX DR N-PSDB; AAK51548.

XX Nucleic acids encoding polypeptides with cytokine-like activities, useful

XX in diagnosis and gene therapy.

XX Claim 20; Page 3306; 6221pp; English.

XX The invention relates to polynucleotides (AAK51456-AAK53435) and the

CC encoded polypeptides (AAM78323-AAK80302) that exhibit activity elating to

CC cytokine, cell proliferation or cell differentiation or which may induce

CC production of other cytokines in other cell populations. The

CC polynucleotides and polypeptides are useful in gene therapy, vaccines or

CC peptide therapy. The polypeptides have various cytokine-like activities,

CC e.g. stem cell growth factor activity, haematopoiesis regulating

CC activity, tissue growth factor activity, immunomodulatory activity and

CC activin/inhibin activity and may be useful in the diagnosis and/or

CC treatment of cancer, leukaemia, nervous system disorders, arthritis and

CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111

CC (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the

CC sequence listing were missing at the time of publication

CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
 CC (AAK52582) and 3666 (AAW80020) are omitted as the relevant pages from the
 CC sequence listing were missing at the time of publication
 XX
 XX
 SQ Sequence 260 AA;

Query Match 97.6%; Score 1197; DB 4; Length 260;
 Best Local Similarity 98.7%; Pred. No. 6.1e-116;
 Matches 220; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 LRAGDSWGMGLACTVWLHPVAPALNRTGDPGPGPSIQKTYDTRYLEHQLRSLAGTYL 62
 DB 38 LPTGDSWGMGLACTVWLHPVAPALNRTGDPGPGPSIQKTYDTRYLEHQLRSLAGTYL 97
 QY 63 NYLGGPPNEPDPNPRLGAEITLPRATVDLEVWRSNDKRLTONYEAYSHLLCYLRGLNR 122
 DB 98 NYLGGPPNEPDPNPRLGAEITLPRATVDLEVWRSNDKRLTONYEAYSHLLCYLRGLNR 157
 QY 123 QNATAELRSLAHFCTSLQGLLSIAGVMAALGYPLPQLPTEPTWTPGPAHSDFLQKM 182
 DB 158 QNATAELRSLAHFCTSLQGLLSIAGVMAALGYPLPQLPTEPTWTPGPAHSDFLQKM 217
 QY 183 DDFWLLKELQTLWRSKDFNRLKKMQPPAAAATVHLGAHGF 225
 DB 218 DDFWLLKELQTLWRSKDFNRLKKMQPPAAAATVHLGAHGF 260

RESULT 12
 AAW56142
 ID AAW56142 standard; protein; 225 AA.
 AC AAW56142;
 DT 13-JUL-1998 (first entry)
 XX Amino acid sequence of murine neurotrophic factor NNT-1.
 DE
 XX Mouse; neurotrophic factor; NNT-1; growth; motor; sympathetic; neuron;
 KW treatment; neurological disease; degeneration; Parkinson's disease;
 KW amyotrophic lateral sclerosis; ALS; Alzheimer's disease; stroke.
 OS Mus sp.
 XX
 XX Key Location/Qualifiers
 FH Peptide 1..27 /note= "signal peptide"
 FT Peptide 28..225
 FT Protein /note= "mature peptide"
 XX
 XX US5741772-A.
 PN
 XX
 XX 21-APR-1998.
 PD
 XX
 XX 03-FEB-1997; 97US-00792019.
 XX
 XX 03-FEB-1997; 97US-00792019.
 XX
 XX (AMGE-) AMGEN INC.
 PA
 XX
 XX Chang M;
 XX
 XX WPI; 1998-260526/23.
 DR
 XX N-PSDB; AAV22654.
 DR
 XX
 XX Neurotrophic factor NNT-1 polypeptide and related nucleic acids - useful
 PT for stimulating growth of motor and sympathetic neurons.
 XX

PS Claim 2; Fig 5; 41pp; English.
 XX
 CC The present sequence represents a murine neurotrophic factor, designated
 CC NNT-1, which is capable of stimulating growth of motor or sympathetic
 CC neurons. The NNT-1 protein is useful in the treatment of neurological
 CC diseases characterised by the degeneration and death of particular
 CC classes of neurons. These diseases specifically include Parkinson's
 CC disease, amyotrophic lateral sclerosis (ALS), Alzheimer's disease, stroke
 CC and various degenerative disorders affecting vision
 XX
 XX
 SQ Sequence 225 AA;

Query Match 97.3%; Score 1193; DB 2; Length 225;
 Best Local Similarity 96.9%; Pred. No. 1.3e-115;
 Matches 218; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDLRAGDSWGMGLACTVWLHPVAPALNRTGDPGPGPSIQKTYDTRYLEHQLRSLAGT 60
 DB 1 MDLRAGDSWGMGLACTVWLHPVAPALNRTGDPGPGPSIQKTYDTRYLEHQLRSLAGT 60
 QY 61 YLYLGGPPNEPDPNPRLGAEITLPRATVDLEVWRSNDKRLTONYEAYSHLLCYLRGL 120
 DB 61 YLYLGGPPNEPDPNPRLGAEITLPRATVDLEVWRSNDKRLTONYEAYSHLLCYLRGL 120
 QY 121 NROQATAELRSLAHFCTSLQGLLSIAGVMAALGYPLPQLPTEPTWTPGPAHSDFLQ 180
 DB 121 NROQATAELRSLAHFCTSLQGLLSIAGVMAALGYPLPQLPTEPTWTPGPAHSDFLQ 180
 QY 181 KMDDFWLLKELQTLWRSKDFNRLKKMQPPAAAATVHLGAHGF 225
 DB 181 KMDDFWLLKELQTLWRSKDFNRLKKMQPPAAAATVHLGAHGF 225

RESULT 13
 AAW29716
 ID AAW29716 standard; protein; 225 AA.
 AC AAW29716;
 DT 09-NOV-1998 (first entry)
 XX Mouse neurotrophic factor NNT-1.
 DE
 XX NNT-1; neurotrophic factor; mouse; antiinflammatory; adjuvant;
 KW Alzheimer's disease; Parkinson's disease; Huntington's disease;
 KW amyotrophic lateral sclerosis; Charcot-Marie-Tooth syndrome;
 KW peripheral neuropathy; dystrophy; neural retina degeneration;
 KW common variable immunodeficiency; CVID; selective IgA deficiency;
 KW hypogammaglobulinaemia; X-linked agammaglobulinaemia; antiseptic;
 KW therapy.
 OS Mus sp.
 XX
 XX Key Location/Qualifiers
 FH Peptide 1..27 /label= Sig_peptide
 FT Peptide 28..225
 FT Protein /label= Mat_protein
 FT
 XX
 XX W09833922-A1.
 PN
 XX
 XX 06-AUG-1998.
 PD
 XX
 XX 02-FEB-1998; 98WO-US002363.
 XX
 XX 03-FEB-1997; 97US-00792019.
 XX 30-JAN-1998; 98US-00016534.
 XX
 XX (AMGE-) AMGEN INC.
 XX
 XX Chang M, Elliot GS, Senaldi G, Sarmiento U;
 XX WPI; 1998-437475/37.
 DR

03-FEB-1997; 97US-00792019.
(AMGE-) AMGEN INC.
Chang M;
WPI; 2000-338492/29.
N-PSTB; AAA39483.

New nucleic acids encoding neurotrophic factors useful for stimulating growth of motor or sympathetic neurons for treating neuron cell damage.

Claim 2b; Fig 5; 42pp; English.

This invention describes a novel nucleic acid molecule (I) encoding a novel neurotrophic factor (NNT-1) (II) which has neurotropic, neuroprotective, anticonvulsant, antiparkinsonian, antidiabetic and ophthalmological activity. (I) is useful for producing NNT-1 polypeptides which are useful for treating patients in whom various cells of the central, autonomic, or peripheral nervous system have degenerated and/or have been damaged by congenital disease, trauma, mechanical damage, surgery, stroke, ischemia, infection, metabolic disease, nutritional deficiency, malignancy and/or toxic agents. NNT-1 proteins are used to treat diseases like Alzheimer's, Parkinson's, amyotrophic lateral sclerosis, Charcot-Marie-Tooth syndrome, Huntington's disease, peripheral neuropathy induced by diabetes or other metabolic disorders, and/or dystrophies or degeneration of the neural retina such as retinitis pigmentosa, drug-induced retinopathies, stationary forms of night blindness, progressive cone-rod degeneration, immune disorders and hematopoietic disorders. (I) is effective in treating neurological conditions and promotes neuron regeneration. Neural functions are effectively restored in patients suffering from various neurological disorders. This sequence represents the murine NNT-1 protein described in the method of the invention

Sequence 225 AA:

Query Match	97.3%;	Score 1193;	DB 3;	Length 225;
Best Local Similarity	96.9%;	Pred. No. 1.3e-115;		
Matches 218;	Conservative 3;	Mismatches 4;	Indels 0;	Gaps 0
QY	1	MDLRAGDSWGMCLACTVWLHPAVPALNRTGDPGGPSIQKTYDITRYLEHQRLSLAGT	60	
Db	1	MDLRAGDSWGMCLACTVWLHPAVPALNRTGDPGGPSIQKTYDITRYLEHQRLSLAGT	60	
QY	61	YNYLGGPFNPBPDPNPRLGAETLPRAVTDLVYWRSLNDKLRTQNYEAYSHLLCYLRGL	120	
Db	61	YNYLGGPFNPBPDPNPRLGAETLPRAVTNLVYWRSLNDKLRTQNYEAYSHLLCYLRGL	120	
QY	121	NQQAATAELRSLSLAHFCTSLOGLIGSGTAGYMAALGYPLPQPLPGTPTTQGPASDFDQ	180	
Db	121	NQQAATAELRSLSLAHFCTSLOGLIGSGTAGYMATGYPLPQPLPGTPTQANAPASDFDQ	180	
QY	181	KMDDFWLLKEIQTLWRSKDFNRLKKXQPPAAAVTLHLGAHGF	225	
Db	181	KMDDFWLLKEIQTLWRSKDFNRLKKXQPPAAASVTLHLGAHGF	225	

RESULT 15	
AAU78177	AAU78177
ID	AAU78177 standard; protein; 225 AA.
XX	XX
AC	AAU78177;
XX	XX
DT	05-JUN-2002 (first entry)
XX	XX
DE	Mouse novel neurotrophic factor NNT1.
XX	XX
KW	Mouse; NNT1; neurotrophic factor; IgE-related disease;
KW	Type I allergic disease; allergic rhinitis; eczema; dermatitis;
KW	pollinosis; asthma; immune disease; cancer; arteriosclerosis;
KW	vascular restenosis; rheumatoid arthritis; psoriatic arthritis;

KW inflammatory arthritis; osteoarthritis; inflammatory joint disease;
KW autoimmune disease; multiple sclerosis; lupus; diabetes; endometriosis;
KW inflammatory bowel disease; transplant rejection; reproductive disorder;
KW graft versus host disease; infertility; miscarriage; preterm labour.

XX

OS Mus sp.

XX WO200215977-A2.

PN 28-FEB-2002.

PD 17-AUG-2001; 2001WO-US025906.

XX 18-AUG-2000; 2000US-0226436P.

XX 16-AUG-2001; 2001US-00931704.

XX (AMGE-) AMGEN INC.

PA Senaldi G;

XX WPI: 2002-280867/32.

XX N-PSDB; ABK11649.

XX Treating Immunoglobulin E-related disease, modulating IgE levels in a

PT patient, preventing IgE-related disease and treating allergic diseases,

PT involves administering NNT-1 inhibitor to a patient.

XX Claim 2; Fig 5; 63pp; English.

XX The invention relates to treating Immunoglobulin E (IgE)-related disease,

CC modulating IgE levels in a patient, preventing an IgE-related disease,

CC and treating allergic diseases, comprising administering a

CC therapeutically effective amount of novel neurotrophic factor (NNT)-1

CC inhibitor to a patient. Also included are a method of diagnosing an IgE-

CC related disease or susceptibility to an IgE-related disease, by

CC determining the presence or amount of expression of an NNT1 polypeptide

CC encoded by a NNT1 nucleotide sequence, its fragment or naturally

CC occurring variant, and diagnosing an IgE-related disease or

CC susceptibility of an IgE-related disease based on the presence or amount

CC of expression of the polypeptide and a pharmaceutical composition for use

CC in treating IgE-related disease, comprising the NNT1 inhibitor. The NNT1

CC inhibitor is useful for preventing and treating IgE-related disease,

CC modulating IgE levels, and treating allergic diseases e.g. Type I

CC allergic disease, allergic rhinitis, eczema, dermatitis, pollinosis,

CC asthma, immune diseases and disorders, diseases involving abnormal cell

CC proliferation including cancer, arteriosclerosis and vascular stenosis,

CC diseases and conditions relating to dysfunction of immune system

CC including rheumatoid arthritis, psoriatic arthritis, inflammatory

CC arthritis, osteoarthritis, inflammatory joint disease, autoimmune

CC disease, multiple sclerosis, lupus, diabetes, inflammatory bowel disease,

CC transplant rejection, and graft versus host disease, and reproductive

CC diseases and disorders including infertility, miscarriage, preterm labour

CC and delivery, and endometriosis. The present sequence represents Mouse

CC NNT1

XX Sequence 225 AA;

XX Query Match 97.3%; Score 1193; DB 5; Length 225;

XX Best Local Similarity 96.9%; Pred. No. 1.3e-115;

XX Matches 218; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDLRAGDSWGMLACTLVHLHPAVPALNRTGDPGPGSIQKTYDLTRYLEHQLRSLAGT 60

Db 1 MDLRAGDSWGMLACTLVHLHPAVPALNRTGDPGPGSIQKTYDLTRYLEHQLRSLAGT 60

QY 61 YLNYLGPPNPNPNPRGAEFTLPRATYDLEWRSNDKRLTONYEAYSHLLCYLRGL 120

Db 61 YLNYLGPPNPNPNPRGAEFTLPRATYDLEWRSNDKRLTONYEAYSHLLCYLRGL 120

QY 121 NRQAATAELRSLAHFCTSLQGLGSIAGVMAALGYPLPQPLPGTEPTWPGFAHSDFLQ 180

Db 121 NRQAATAELRSLAHFCTSLQGLGSIAGVMAALGYPLPQPLPGTEPTWPGFAHSDFLQ 180

QY 181 KMDDFWLLKELQTLWRSKADFNRLKKKQKQPPAAAVTLHLGAHGF 225

Db 181 KMDDFWLLKELQTLWRSKADFNRLKKKQKQPPAAAVTLHLGAHGF 225

Search completed: August 10, 2004, 06:45:59
Job time : 51 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 10, 2004, 06:46:33 ; Search time 513 Seconds
(without alignments)
137.580 Million cell updates/sec

Title: US-09-931-704-2

Perfect score: 1226
Sequence: 1 MDLRAGDSWGMACLTCTVLM.....KKKQPPAAAVTLHGAGF 225

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1291235 seqs, 313682936 residues

Total number of hits satisfying chosen parameters: 1291235

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
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8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09E_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_NEW_PUB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1226	100.0	225	9	US-09-931-704-2
2	1226	100.0	225	14	US-10-212-793-2
3	1226	100.0	225	16	US-10-408-765A-785
4	1226	100.0	253	12	US-10-236-115-1346
5	1204	98.2	321	12	US-10-276-774-2266
6	1193	97.3	225	9	US-09-931-704-5
7	885	72.2	164	9	US-09-864-761-40014
8	124.5	10.2	203	14	US-10-212-793-3
9	118.5	9.7	203	9	US-09-896-856-3
10	118.5	9.7	203	14	US-10-107-931-3
11	118.5	9.7	203	15	US-10-407-303-3
12	118.5	9.7	203	16	US-10-722-095-3
13	105	8.6	471	12	US-10-282-122A-69553
14	96.5	7.9	243	9	US-09-810-052-5
15	96.5	7.9	243	10	US-09-791-497-8

16	96.5	7.9	243	13	US-10-000-776-6	Sequence 6, Appli
17	92.5	7.5	860	14	US-10-156-761-11445	Sequence 11445, A
18	91.5	7.5	201	9	US-09-901-540-3	Sequence 3, Appli
19	91.5	7.5	201	9	US-09-896-856-8	Sequence 8, Appli
20	91.5	7.5	201	9	US-09-901-257-3	Sequence 3, Appli
21	91.5	7.5	201	14	US-10-107-931-8	Sequence 8, Appli
22	91.5	7.5	201	14	US-10-212-793-4	Sequence 4, Appli
23	91.5	7.5	201	15	US-10-407-303-8	Sequence 8, Appli
24	91.5	7.5	201	16	US-10-722-095-8	Sequence 8, Appli
25	91.5	7.5	693	16	US-10-452-858C-93	Sequence 93, Appli
26	91.5	7.5	1182	14	US-10-024-368-6	Sequence 6, Appli
27	91	7.4	195	9	US-09-770-361-5	Sequence 5, Appli
28	91	7.4	195	14	US-10-226-759-5	Sequence 5, Appli
29	91	7.4	195	14	US-10-281-643-5	Sequence 5, Appli
30	91	7.4	195	15	US-10-383-916-5	Sequence 5, Appli
31	91	7.4	242	10	US-09-791-497-2	Sequence 2, Appli
32	91	7.4	242	13	US-10-000-776-2	Sequence 2, Appli
33	90	7.3	232	9	US-09-810-052-2	Sequence 2, Appli
34	89.5	7.3	1313	12	US-10-437-421-22	Sequence 22, Appli
35	88.5	7.2	319	12	US-10-425-114-61252	Sequence 61252, A
36	88.5	7.2	323	12	US-10-425-114-38754	Sequence 38754, A
37	88.5	7.2	1429	12	US-10-029-347-3	Sequence 3, Appli
38	88.5	7.2	1429	14	US-10-028-374-3	Sequence 3, Appli
39	88.5	7.2	1429	14	US-10-183-770-3	Sequence 3, Appli
40	87.5	7.1	1207	14	US-10-024-368-5	Sequence 5, Appli
41	85.5	7.0	499	12	US-10-425-114-45547	Sequence 45547, A
42	85.5	7.0	1022	12	US-10-188-186-26	Sequence 26, Appli
43	85	6.9	727	15	US-10-231-913-88	Sequence 98, Appli
44	84.5	6.9	389	15	US-10-369-493-42941	Sequence 22941, A
45	84.5	6.9	1473	12	US-10-182-822A-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1

US-09-931-704-2
; Sequence 2, Application US/09931704
; Patent No. US20020041873A1
; GENERAL INFORMATION:
; APPLICANT: Senaldi, Giorgio
; TITLE OF INVENTION: Methods and Compositions for Treating IgE-Related Disease Using N
; TITLE OF INVENTION: Inhibitors
; FILE REFERENCE: A-695
; CURRENT APPLICATION NUMBER: US/09/931,704
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: US 60/226,436
; PRIOR FILING DATE: 2000-08-18
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-931-704-2

Query Match	100.0%;	Score 1226;	DB 9;	Length 225;
Best Local Similarity	100.0%;	Pred. No. 8.8e-115;		
Matches 225;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MDLRAGDSWGMACLTCTVLMWLPVAPALNRTGDPGPGSIQKTYDITRYLHQLRLSLACT	60	
Db	1	MDLRAGDSWGMACLTCTVLMWLPVAPALNRTGDPGPGSIQKTYDITRYLHQLRLSLACT	60	
Qy	61	YLYNLGPPNEPDPFPRILGAETLPRATVDLEWVRSNDKRLTQNYEAYSHLLCYLRGL	120	
Db	61	YLYNLGPPNEPDPFPRILGAETLPRATVDLEWVRSNDKRLTQNYEAYSHLLCYLRGL	120	
Qy	121	NROQATAEIARRSLAHFCTSLQGLLSIAGVMAALGYPLPOPLPGTEPTWTPGPAHSDFLQ	180	
Db	121	NROQATAEIARRSLAHFCTSLQGLLSIAGVMAALGYPLPOPLPGTEPTWTPGPAHSDFLQ	180	
Qy	181	KMDDFWLLKELQTLWRSKDFNRLKKKQPPAAAVTLHGAGF	225	

Db 181 KMDDFWLLKELQTLWLRSAKDFNRLKKMKQPPAAAVTLHLGAHGF 225
|||||

RESULT 2

US-10-212-793-2
; Sequence 2, Application US/10212793
; Publication No. US20030087395A1
; GENERAL INFORMATION:
; APPLICANT: Shi et al.
; TITLE OF INVENTION: Cardiotrophin-Like Cytokine
; FILE REFERENCE: EP385D1C1
; CURRENT APPLICATION NUMBER: US/10/212,793
; CURRENT FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: US 09/438,299
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 09/106,182
; PRIOR FILING DATE: 1998-06-29
; PRIOR APPLICATION NUMBER: US 60/051,311
; PRIOR FILING DATE: 1997-06-30
; NUMBER OF SEQ ID NOS: 24
; SEQ ID NO 2
; LENGTH: 225
; TYPE: PRT
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: signal
; LOCATION: (-27)..(-1)
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(198)
US-10-212-793-2

Query Match 100.0%; Score 1226; DB 14; Length 225;
Best Local Similarity 100.0%; Pred. No. 8.8e-115;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDLRAGDSWGMCLACTVWLWHPAVPALNRTGDPGPGPSIQKTYDLYLRYLHQLRSLAGT 60
DB 1 MDLRAGDSWGMCLACTVWLWHPAVPALNRTGDPGPGPSIQKTYDLYLRYLHQLRSLAGT 60
QY 61 YLNYLGPPFPNEPDPNPRLLGAETLPATVDLEVWRSNDKRLTQNYEAYSHLLCYLRGL 120
DB 61 YLNYLGPPFPNEPDPNPRLLGAETLPATVDLEVWRSNDKRLTQNYEAYSHLLCYLRGL 120
QY 121 NRQAATAELRRSLAHFCTSLQGLLSIAGVMAALGYPLPQPLPGTEPTWTPGPAHSDFLQ 180
DB 121 NRQAATAELRRSLAHFCTSLQGLLSIAGVMAALGYPLPQPLPGTEPTWTPGPAHSDFLQ 180
QY 181 KMDDFWLLKELQTLWLRSAKDFNRLKKMKQPPAAAVTLHLGAHGF 225
DB 181 KMDDFWLLKELQTLWLRSAKDFNRLKKMKQPPAAAVTLHLGAHGF 225

RESULT 3

US-10-408-765A-785
; Sequence 785, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 785
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-785

Query Match 100.0%; Score 1226; DB 16; Length 225;
Best Local Similarity 100.0%; Pred. No. 8.8e-115;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDLRAGDSWGMCLACTVWLWHPAVPALNRTGDPGPGPSIQKTYDLYLRYLHQLRSLAGT 60
DB 1 MDLRAGDSWGMCLACTVWLWHPAVPALNRTGDPGPGPSIQKTYDLYLRYLHQLRSLAGT 60
QY 61 YLNYLGPPFPNEPDPNPRLLGAETLPATVDLEVWRSNDKRLTQNYEAYSHLLCYLRGL 120
DB 61 YLNYLGPPFPNEPDPNPRLLGAETLPATVDLEVWRSNDKRLTQNYEAYSHLLCYLRGL 120
QY 121 NRQAATAELRRSLAHFCTSLQGLLSIAGVMAALGYPLPQPLPGTEPTWTPGPAHSDFLQ 180
DB 121 NRQAATAELRRSLAHFCTSLQGLLSIAGVMAALGYPLPQPLPGTEPTWTPGPAHSDFLQ 180
QY 181 KMDDFWLLKELQTLWLRSAKDFNRLKKMKQPPAAAVTLHLGAHGF 225
DB 181 KMDDFWLLKELQTLWLRSAKDFNRLKKMKQPPAAAVTLHLGAHGF 225

RESULT 4

US-10-296-115-1346
; Sequence 1346, Application US/10296115
; Publication No. US20040053248A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: No. US20040053248A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 784PCT
; CURRENT APPLICATION NUMBER: US/10/296,115
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 1478
; SEQ ID NO 1346
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-296-115-1346

Query Match 100.0%; Score 1226; DB 12; Length 253;
Best Local Similarity 100.0%; Pred. No. 1e-114;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDLRAGDSWGMCLACTVWLWHPAVPALNRTGDPGPGPSIQKTYDLYLRYLHQLRSLAGT 60
DB 29 MDLRAGDSWGMCLACTVWLWHPAVPALNRTGDPGPGPSIQKTYDLYLRYLHQLRSLAGT 88
QY 61 YLNYLGPPFPNEPDPNPRLLGAETLPATVDLEVWRSNDKRLTQNYEAYSHLLCYLRGL 120
DB 89 YLNYLGPPFPNEPDPNPRLLGAETLPATVDLEVWRSNDKRLTQNYEAYSHLLCYLRGL 148
QY 121 NRQAATAELRRSLAHFCTSLQGLLSIAGVMAALGYPLPQPLPGTEPTWTPGPAHSDFLQ 180
DB 149 NRQAATAELRRSLAHFCTSLQGLLSIAGVMAALGYPLPQPLPGTEPTWTPGPAHSDFLQ 208
QY 181 KMDDFWLLKELQTLWLRSAKDFNRLKKMKQPPAAAVTLHLGAHGF 225
DB 209 KMDDFWLLKELQTLWLRSAKDFNRLKKMKQPPAAAVTLHLGAHGF 253

RESULT 5

US-10-276-774-2266
; Sequence 2266, Application US/10276774
; Publication No. US20040053245A1

GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang, Y, Tom et al
; TITLE OF INVENTION: 21272-030
; FILE REFERENCE: 21272-030
; CURRENT APPLICATION NUMBER: US/10/276,774
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 2700
; SOFTWARE: Custom
; SEQ ID NO 2266
; LENGTH: 321
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-276-774-2266

Query Match 98.2%; Score 1204; DB 12; Length 321;
Best Local Similarity 99.1%; Pred. No. 2.3e-112; Indels 0; Gaps 0;
Matches 221; Conservative 0; Mismatches 2;

Qy 3 LRAGDSWGLACLTCTVLMHLPVAPALNRTGDPGPGSIQKTYDLTRYLEHQLSLAGTYL 62
Db 99 LPTGDSWGLACLTCTVLMHLPVAPALNRTGDPGPGSIQKTYDLTRYLEHQLSLAGTYL 159

Qy 63 NYLGGPPNPPNPPRIGAEPLPRATVDLEWRSNDKRLRTQNYEAYSHLLCYLRGLNR 122
Db 159 NYLGGPPNPPNPPRIGAEPLPRATVDLEWRSNDKRLRTQNYEAYSHLLCYLRGLNR 218

Qy 123 QAATAELRRSLAHFCTSLQGLLSIAGVMAALGYPLPQPLPGTEPTWTPGPAHSDFLQ 182
Db 219 QAATAELRRSLAHFCTSLQGLLSIAGVMAALGYPLPQPLPGTEPTWTPGPAHSDFLQ 278

Qy 183 DDFWLLKELQTLWRSKADFNRLKKKQPPAAAATVHLGAHGF 225
Db 279 DDFWLLKELQTLWRSKADFNRLKKKQPPAAAATVHLGAHGF 321

RESULT 6
US-09-931-704-5
; Sequence 5, Application US/09931704
; Patent No. US20020041873A1
; GENERAL INFORMATION:
; APPLICANT: Senaldi, Giorgio
; TITLE OF INVENTION: Methods and Compositions for Treating IGB-Related Disease Using N
; FILE REFERENCE: A-695
; CURRENT APPLICATION NUMBER: US/09/931,704
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: US 60/226,436
; PRIOR FILING DATE: 2000-08-18
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 5
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Murine
US-09-931-704-5

Query Match 97.3%; Score 1193; DB 9; Length 225;
Best Local Similarity 96.9%; Pred. No. 1.8e-111; Indels 0; Gaps 0;
Matches 218; Conservative 3; Mismatches 4;

Qy 1 MDLRAGDSWGLACLTCTVLMHLPVAPALNRTGDPGPGSIQKTYDLTRYLEHQLSLAGT 60
Db 1 MDLRAGDSWGLACLTCTVLMHLPVAPALNRTGDPGPGSIQKTYDLTRYLEHQLSLAGT 60

Qy 61 YLYNLGPPNPPNPPRIGAEPLPRATVDLEWRSNDKRLRTQNYEAYSHLLCYLRGL 120
Db 61 YLYNLGPPNPPNPPRIGAEPLPRATVDLEWRSNDKRLRTQNYEAYSHLLCYLRGL 120

Qy 121 NRQAATAELRRSLAHFCTSLQGLLSIAGVMAALGYPLPQPLPGTEPTWTPGPAHSDFLQ 180
Db 121 NRQAATAELRRSLAHFCTSLQGLLSIAGVMAALGYPLPQPLPGTEPTWTPGPAHSDFLQ 180

Qy 181 KMDDFWLLKELQTLWRSKADFNRLKKKQPPAAAATVHLGAHGF 225
Db 181 KMDDFWLLKELQTLWRSKADFNRLKKKQPPAAAATVHLGAHGF 225

RESULT 7
US-09-864-761-40014
; Sequence 40014, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aemica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 40014
; LENGTH: 164
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC005849.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 4.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.4
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4.2

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; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4.4
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4.5
; OTHER INFORMATION: EST. HUMAN HIT: A1752561.1, EVALUE 3.00e-66
; OTHER INFORMATION: SWISSPROT HIT: Q63086, EVALUE 8.00e-03
US-09-864-761-40014

Query Match      72.2%; Score 885; DB 9; Length 164;
Best Local Similarity 99.4%; Pred. No. 1.1e-80;
Matches 163; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 62 LNYLGGPPFNPDPNPRGLAETLPRTATVDEWRSNDKRLRTONYEASHLLCYLRGLN 121
Db 1 LNYLGGPPFNPDPNPRGLAETLPRTATVDEWRSNDKRLRTONYEASHLLCYLRGLN 60

Qy 122 RQATAELESLAHFCTSLQGLLGSAGVMAALGYPLPQPLGTETPTWPGPAHSDFLQK 181
Db 61 RQATAELESLAHFCTSLQGLLGSAGVMAALGYPLPQPLGTETPTWPGPAHSDFLQK 120

Qy 182 MDDFWLLKELQTLWRSKDFNRLKKKMPPPAAAVTLHLGAHGF 225
Db 121 MDDFWLLKELQTLWRSKDFNRLKKKMPPPAAAVTLHLGAHGF 164

RESULT 8
US-10-212-793-3
; Sequence 3, Application US/10212793
; Publication No. US20030087395A1
; GENERAL INFORMATION:
; APPLICANT: Shi et al.
; TITLE OF INVENTION: Cardiostrophin-Like Cytokine
; FILE REFERENCE: PF385D1C1
; CURRENT APPLICATION NUMBER: US/10/212,793
; PRIOR FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: US 09/438,299
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 09/106,182
; PRIOR FILING DATE: 1998-06-29
; PRIOR APPLICATION NUMBER: US 60/051,311
; PRIOR FILING DATE: 1997-06-30
; NUMBER OF SEQ ID NOS: 24
; SEQ ID NO 3
; TYPE: PRT
; ORGANISM: rattus norvegicus
US-10-212-793-3

Query Match      10.2%; Score 124.5; DB 14; Length 203;
Best Local Similarity 28.1%; Pred. No. 0.00041;
Matches 50; Conservative 24; Mismatches 85; Indels 19; Gaps 5;

Qy 40 IQKTYDLTRYLEHQLRSAGTYLNYLGGPPFNPDPNPPRL---GAETLPRTATVDEWRS 96
Db 27 IROTHNLARLLTKYADQLLEEYVQQQGEFGLPGFPPRLPLAGLSGPAPSHAGLPV--- 83

Qy 97 LNDKRLTONYEASHLLCYLRGLNRQAA-----TAELESLAHFCTSLQGLLGSAGV 151
Db 84 ---SERLRQDAALSLPALLDAVRRRQAELEPNRAPRLRLSLDEAARQVRLGAATVTL 140

Qy 152 AALGY----PLQPLPGTETPTWPGPAHSDFLQKDDFWLLKELQTLWRSKDFNRL 205
Db 141 AALGAARGPVPEPV-ATSALETSNSAGVFSKVLGLHVCGLYGEWVSRTEGDLGQL 197

RESULT 9
US-09-896-856-3
; Sequence 3, Application US/09896856
; Patent No. US20020137189A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Joffre
; Chien, Kenneth
; King, Kathleen
; Pennica, Diane
; Wood, William

```

```

; TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses Therefor
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/896,856
; FILING DATE: 29-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/733,850
; FILING DATE: 18-OCT-1996
; APPLICATION NUMBER: US 08/471,112
; FILING DATE: 06-JUN-1995
; APPLICATION NUMBER: 08/233,609
; FILING DATE: 25-APR-1994
; APPLICATION NUMBER: 08/286304
; FILING DATE: 05-AUG-1994
; APPLICATION NUMBER: 08/443129
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Conley, Deirdre L.
; REGISTRATION NUMBER: 36,487
; REFERENCE/DOCKET NUMBER: P0894P1D2C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-2066
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 203 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-896-856-3

Query Match      9.7%; Score 118.5; DB 9; Length 203;
Best Local Similarity 28.8%; Pred. No. 0.0016;
Matches 51; Conservative 21; Mismatches 88; Indels 17; Gaps 5;

Qy 40 IQKTYDLTRYLEHQLRSAGTYLNYLGGPPFNPDPNPPRL---GAETLPRTATVDEWRS 96
Db 27 IROTHNLARLLTKYADQLLEEYVQQQGEFGLPGFPPRLPLAGLSGPAPSHAGLPV--- 83

Qy 97 LNDKRLTONYEASHLLCYLRGLNRQAA-----TAELESLAHFCTSLQGLLGSAGV 151
Db 84 ---SERLRQDAALSLPALLDAVRRRQAELEPNRAPRLRLSLDEAARQVRLGAATVTL 140

Qy 152 AALGYPL--PQPLPGTETPTWPGPAHSDFLQKDDFWLLKELQTLWRSKDFNRL 205
Db 141 AALGAARGPVPEPVTVATLTFTANSTAGIFSAXVLGHVCGLYGEWVSRTEGDLGQL 197

RESULT 10
US-10-107-931-3
; Sequence 3, Application US/10107931
; Publication No. US20030054550A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Joffre
; Chien, Kenneth
; King, Kathleen
; Pennica, Diane
; Wood, William
; TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses Therefor

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QY 97 LNDKRLTQNYEAYSHLLCYLRGLNRQA-----TAELRRSLAHFCTSLQGLLGIAGVM 151
Db 84 --SERLRQDAALSVLPALLDAVRRQALNPRAPRLLSLEDAARQVRAALGAAYETVL 140
QY 152 AALGYPIL--POPPLGTEPT-WTPGPAHSDFLOKMDDFWLLKELOTWLRSAKDFNEL 205
Db 141 AALGAARAGPGPEVTVATLFTANSTAGIFSAKVLGFHVGLGYENVSRTGDLQGL 197

RESULT 13

US-10-282-122A-69553
; Sequence 69553, Application US/10282122A
; Publication No. US2004009129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohsen, Karl
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 69553
; LENGTH: 471
; TYPE: PRT
; ORGANISM: Pseudomonas syringae

US-10-282-122A-69553

Query Match 8.6%; Score 105; DB 12; Length 471;
Best Local Similarity 25.0%; Pred. No. 0.11;
Matches 53; Conservative 15; Mismatches 98; Indels 46; Gaps 6;

QY 1 MDLRAGDSWGLACICTVLMHLPVAPALNRGTGDPGPGPSIQKTYDTRYLEHQLRSLAGT 60
Db 182 LELREGDPAALLEAAELAAATLPLMPC-----DISKAERYLLDASSYLS-- 228
QY 61 YNLYLGPFPNPDNPPPLGTHETLPRAVDLEVRSLNDRKRLTQNTVEYSH----- 112
Db 229 -----LPAPTNATETPLDDAYSALAWHLGSSQRDLAEQYRFNGHWELLODW 275
QY 113 -LLCYLRGLNRQAATAELRRSLAHFCTSLQGLLGIAGVMALGYPPLPPLPGTEPTWP 171

Db 276 EMLGELRALTSSLGQAAPRTSTAQIRTAIDALLLED-----WRPLVQ--AGQEDADVR 325
QY 172 GPAHSDFLOKMDDF-WLLKELOTWLRSAKDF 202
Db 326 GAAHEQFLEELQDTRWGEFSLNTRWLLARSW 357

RESULT 14

US-09-810-052-5
; Sequence 5, Application US/09810052
; Patent No. US20020009775A1
; GENERAL INFORMATION:
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Presnell, Scott R.
; TITLE OF INVENTION: HELICAL PROTEIN ZALPHA51
; FILE REFERENCE: 00-24
; CURRENT APPLICATION NUMBER: US/09/810,052
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/190,410
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/199,443
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-810-052-5

Query Match 7.9%; Score 96.5; DB 9; Length 243;
Best Local Similarity 23.7%; Pred. No. 0.34;
Matches 58; Conservative 26; Mismatches 104; Indels 57; Gaps 9;

QY 1 MDLRAGD-SWGLACICTVLMHLPVAPALNRGTGDPGPGPSIQK-----TYDL 46
Db 1 MGQTAGDLGWRLSLLLLPLLLVQAGVWGFPFPPG-----RPQLSELREFTVSLHL 53
QY 47 TRYLEHQLRSLAGTYLN-----YLGPPFPNPDNPPPLGTHETLPRAVDLEVRSLN 98
Db 54 ARKLLSEVRGQAHRAESHLPGVNLVLLP-----LG-EQLPDSVSLTFQAWRRLS 101
QY 99 DKRLTQNYEAYSHLLCYLRGLNRQAATAELRR-SLAHFTSLQGLLGIAGVMALGYP 157
Db 102 DPERLCFISTTIQFPFAPGGTQGRWTNMRMQLWAMRLDLRLQHLRFQVLAAGFN 161
QY 158 LPQP-----LPGTEPTWTPGPAHSDFLOKMDDFWLLKELOTWLRSAKDF 202
Db 162 LPEEEEEEEEEEEEERKGLLPGALGSAIQPAQVSWPQLSTYRLLSHLSLVLRAVREL 221
QY 203 NRLKK 207
Db 222 LLLSK 226

RESULT 15

US-09-791-497-8
; Sequence 8, Application US/09791497
; Publication No. US20030008343A1
; GENERAL INFORMATION:
; APPLICANT: Timans, Jacqueline C.
; APPLICANT: Kastelein, Robert A.
; APPLICANT: Bazan, J. Fernando
; APPLICANT: Pefanz, Stefan
; TITLE OF INVENTION: Mammalian Cytokines; Related Reagents
; FILE REFERENCE: DX01040K2
; CURRENT APPLICATION NUMBER: US/09/791,497
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 09/627,897
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: 60/146,581
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 60/147,763

; PRIOR FILING DATE: 1999-08-06
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin ver. 2.0
; SEQ ID NO 8
; LENGTH: 243
; TYPE: PRT
; ORGANISM: primate; surmised Homo sapiens
US-09-791-497-8

Query Match 7.9%; Score 96.5; DB 10; Length 243;
Best Local Similarity 23.7%; Pred. No. 0.34;
Matches 58; Conservative 26; Mismatches 104; Indels 57; Gaps 9;
QY 1 MDLRAGD-SWGMACLCCTVL-----WHLPAVPALNRTGDPGPGSIQK-----TYDL 46
Db 1 MCQTAGDLGWRLLSLLLLLVQAGVWGFPFPPG-----RPQISIQELRREFTVSLHL 53
QY 47 TRYLEHQRLSLAGTYLN-----YLGPPFNEPDPFNPRLGAETLPRATVVDLEWRSLN 98
Db 54 ARKLLSEVRGQAHRAFAESHLPQVNLVLLP-----LG-EQLPDVSLTFQAWERLS 101
QY 99 DKLRITQNYEAYSHLLCYLRGIRNQATAELRR-SLAHFCTSLQGLGSIAGVWALGYP 157
Db 102 DPERLCFTSTTLOPFHAPLGGLTQGRWNTNWMQLWAMRLDLRLDQRLHFRFQVLAAGFN 161
QY 158 LPQP-----LFCGTEFTWTPGPAHSDFLQKMDDFWLLXELQTLWRSAXDF 202
Db 162 LPEEEEEEEEEERKGLLPALGSLAQGPQVSWPQLLSTYRLLHSLEIVLSRAVREL 221
QY 203 NRLKK 207
Db 222 LLLSX 226

Search completed: August 10, 2004, 07:12:34
Job time : 515 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 10, 2004, 06:43:28 ; Search time 15 Seconds
(without alignments)
774.390 Million cell updates/sec

Title: US-09-931-704-2
Perfect score: 1226
Sequence: 1 MDLRAGDSWGMGLACTVLW.....KKMQPPAAAVTLHGAGHF 225

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
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2: /cgm2_6/ptodata/2/iaa/5B COMB.pap.*
3: /cgm2_6/ptodata/2/iaa/6A COMB.pap.*
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5: /cgm2_6/ptodata/2/iaa/PCTUS COMB.pap.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1226	100.0	225	1	US-08-792-019B-2
2	1226	100.0	225	3	US-09-106-182-2
3	1226	100.0	225	3	US-08-988-819-2
4	1226	100.0	225	1	US-09-016-534-2
5	1193	97.3	225	1	US-08-792-019B-5
6	1193	97.3	225	3	US-08-988-819-5
7	1193	97.3	225	3	US-09-016-534-5
8	124.5	10.2	203	3	US-09-106-182-3
9	118.5	9.7	203	1	US-08-233-609-3
10	118.5	9.7	203	1	US-08-444-083-3
11	118.5	9.7	203	1	US-08-286-304-3
12	118.5	9.7	203	1	US-08-442-745-3
13	118.5	9.7	203	1	US-08-443-129-3
14	118.5	9.7	203	1	US-08-443-952-3
15	118.5	9.7	203	1	US-08-443-130-3
16	118.5	9.7	203	3	US-08-898-911-3
17	118.5	9.7	203	5	PCT-US95-04467-3
18	91.5	7.5	201	1	US-08-444-083-8
19	91.5	7.5	201	1	US-08-286-304-8
20	91.5	7.5	201	1	US-08-442-745-8
21	91.5	7.5	201	1	US-08-443-129-8
22	91.5	7.5	201	1	US-08-443-952-8
23	91.5	7.5	201	1	US-08-443-130-8
24	91.5	7.5	201	1	US-08-792-019B-11
25	91.5	7.5	201	3	US-09-106-182-4
26	91.5	7.5	201	3	US-08-988-819-11
27	91.5	7.5	201	3	US-08-898-911-8

28	91.5	7.5	201	3	US-09-016-534-11	Sequence 11, Appli
29	91.5	7.5	201	4	US-09-648-183-3	Sequence 3, Appli
30	91.5	7.5	201	5	PCT-US95-04467-8	Sequence 8, Appli
31	91.5	7.5	1182	4	US-09-287-354-6	Sequence 6, Appli
32	91	7.4	195	1	US-07-959-284-5	Sequence 5, Appli
33	91	7.4	195	2	US-08-308-736A-5	Sequence 5, Appli
34	91	7.4	195	4	US-08-645-107A-5	Sequence 5, Appli
35	91	7.4	195	4	US-09-197-349-5	Sequence 5, Appli
36	91	7.4	195	4	US-09-031-693-5	Sequence 5, Appli
37	91	7.4	195	4	US-09-454-380-5	Sequence 5, Appli
38	91	7.4	195	5	PCT-US92-08258-2	Sequence 2, Appli
39	91	7.4	195	5	PCT-US93-09649A-5	Sequence 5, Appli
40	91	7.4	195	5	PCT-US93-09649-5	Sequence 5, Appli
41	89	7.3	737	4	US-09-252-991A-22539	Sequence 22539, A
42	87.5	7.1	1207	4	US-09-287-354-5	Sequence 5, Appli
43	85.5	7.0	560	2	US-08-756-317-11	Sequence 11, Appli
44	84.5	6.9	426	4	US-09-252-991A-29288	Sequence 29288, A
45	84	6.9	200	3	US-08-949-155-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-08-792-019B-2
; Sequence 2, Application US/08792019B
; Patent No. 5741772
; GENERAL INFORMATION:
; APPLICANT: CHANG, MING-SHI
; TITLE OF INVENTION: THE NEUROTROPHIC FACTOR NNT-1
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMGEN INC.
; STREET: 1840 DEHAVILLAND DRIVE
; CITY: THOUSAND OAKS
; STATE: CA
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/792,019B
; FILING DATE: 03-FEB-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: COOK, ROBERT R.
; REGISTRATION NUMBER: 31,602
; REFERENCE/DOCKET NUMBER: A-442
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 225 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-792-019B-2

Query Match	100.0%;	Score 1226;	DB 1;	Length 225;
Best Local Similarity	100.0%;	Pred. No. 2.8e-129;		
Matches 225;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MDLRAGDSWGMGLACTVLWHLPAVPAALNRTGDPGPGPSIQKTYDITRYLEHQLRSLAGT	60	
Db	1	MDLRAGDSWGMGLACTVLWHLPAVPAALNRTGDPGPGPSIQKTYDITRYLEHQLRSLAGT	60	
QY	61	YLNLYGPPFNEPDPNPRILGAETLPATVDLEWRSNDKRLTQNYEAYSHLLCYLRGL	120	
Db	61	YLNLYGPPFNEPDPNPRILGAETLPATVDLEWRSNDKRLTQNYEAYSHLLCYLRGL	120	
QY	121	NROQATAEIARRSLAHCTSIQGLLSIAGVMAALGPIQPLPGCTEPTTTPGPAHSDFLQ	180	

Db 121 NROAATAELRSLAHFCTSLQGLLSIAGVMAALGYPLPQPLPGTPTWTPGPAHSDFLQ 180

Qy 181 KMDDFWLLKELQTLWRSKDFNRLKKMKQPPAAAATLHLGAHGF 225

Db 181 KMDDFWLLKELQTLWRSKDFNRLKKMKQPPAAAATLHLGAHGF 225

RESULT 2

US-09-106-182-2

Sequence 2, Application US/09106182

Patent No. 6046035

GENERAL INFORMATION:

APPLICANT: Shi, Yangu

APPLICANT: Ruben, Steve

TITLE OF INVENTION: Cardiotrophin-Like Cytokine

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc

STREET: 9410 Key West Ave

CITY: Rockville

STATE: MD

COUNTRY: US

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/106,182

FILING DATE: Herewith

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/051,053

FILING DATE: 30-JUN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Brookes, A. Anders

REGISTRATION NUMBER: 36,373

REFERENCE/DOCKET NUMBER: PF385

TELECOMMUNICATION INFORMATION:

TELEPHONE: 301-309-8504

TELEFAX: 301-309-8439

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 225 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-106-182-2

Query Match 100.0%; Score 1226; DB 3; Length 225;

Best Local Similarity 100.0%; Pred. No. 2.8e-129;

Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDLRAGDSWGLACLTVLWHLPAVPAALNRTGDPGPGPSIQKTYDLYLHQLRSLAGT 60

Db 1 MDLRAGDSWGLACLTVLWHLPAVPAALNRTGDPGPGPSIQKTYDLYLHQLRSLAGT 60

Qy 61 YLNYLGPPFNEPDPNPRILGAETLPRATVDLEVWRSNDKRLTQNYEAYSHLLCYLRGL 120

Db 61 YLNYLGPPFNEPDPNPRILGAETLPRATVDLEVWRSNDKRLTQNYEAYSHLLCYLRGL 120

Qy 121 NROAATAELRSLAHFCTSLQGLLSIAGVMAALGYPLPQPLPGTPTWTPGPAHSDFLQ 180

Db 121 NROAATAELRSLAHFCTSLQGLLSIAGVMAALGYPLPQPLPGTPTWTPGPAHSDFLQ 180

Qy 181 KMDDFWLLKELQTLWRSKDFNRLKKMKQPPAAAATLHLGAHGF 225

Db 181 KMDDFWLLKELQTLWRSKDFNRLKKMKQPPAAAATLHLGAHGF 225

RESULT 3

US-08-988-819-2

Sequence 2, Application US/08988819

Patent No. 6054294

GENERAL INFORMATION:

APPLICANT: CHANG, MING-SHI

TITLE OF INVENTION: NEUROTROPHIC FACTOR NNT-1

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: AMGEN INC.

STREET: ONE AMGEN CENTER DRIVE

CITY: THOUSAND OAKS

STATE: CA

COUNTRY: USA

ZIP: 91320

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/988,819

FILING DATE: 12-DEC-1997

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/792,019

FILING DATE: 03-FEB-1997

ATTORNEY/AGENT INFORMATION:

NAME: COOK, ROBERT R.

REGISTRATION NUMBER: 31,602

REFERENCE/DOCKET NUMBER: A-442A

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 225 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-988-819-2

Query Match 100.0%; Score 1226; DB 3; Length 225;

Best Local Similarity 100.0%; Pred. No. 2.8e-129;

Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDLRAGDSWGLACLTVLWHLPAVPAALNRTGDPGPGPSIQKTYDLYLHQLRSLAGT 60

Db 1 MDLRAGDSWGLACLTVLWHLPAVPAALNRTGDPGPGPSIQKTYDLYLHQLRSLAGT 60

Qy 61 YLNYLGPPFNEPDPNPRILGAETLPRATVDLEVWRSNDKRLTQNYEAYSHLLCYLRGL 120

Db 61 YLNYLGPPFNEPDPNPRILGAETLPRATVDLEVWRSNDKRLTQNYEAYSHLLCYLRGL 120

Qy 121 NROAATAELRSLAHFCTSLQGLLSIAGVMAALGYPLPQPLPGTPTWTPGPAHSDFLQ 180

Db 121 NROAATAELRSLAHFCTSLQGLLSIAGVMAALGYPLPQPLPGTPTWTPGPAHSDFLQ 180

Qy 181 KMDDFWLLKELQTLWRSKDFNRLKKMKQPPAAAATLHLGAHGF 225

Db 181 KMDDFWLLKELQTLWRSKDFNRLKKMKQPPAAAATLHLGAHGF 225

RESULT 4

US-09-016-534-2

Sequence 2, Application US/09016534

Patent No. 6143874

GENERAL INFORMATION:

APPLICANT: CHANG, MING-SHI

APPLICANT: ELLIOTT, GARY S.

APPLICANT: SARMIENTO, ULLA

APPLICANT: SENALDI, GIORGIO

TITLE OF INVENTION: THE NEUROTROPHIC FACTOR NNT-1

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: AMGEN INC.

STREET: ONE AMGEN CENTER

CITY: THOUSAND OAKS


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; STATE: CA
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,534
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/792,019
; FILING DATE: 03-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: COOK, ROBERT R.
; REGISTRATION NUMBER: 31,602
; REFERENCE/DOCKET NUMBER: A-442B
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 225 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-016-534-2

Query Match 100.0%; Score 1226; DB 3; Length 225;
Best Local Similarity 100.0%; Pred. No. 2.8e-129;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLRAGDSWGLACICTVLWHLPAVPALNRTGDPGPGSIQKTYDLTRYLEHQLRSLAGT 60
DB 1 MDLRAGDSWGLACICTVLWHLPAVPALNRTGDPGPGSIQKTYDLTRYLEHQLRSLAGT 60
QY 61 YLNYLGPPFPNEPDPNPPRLGAETLPRATVDLEWVRSNDKRLTQNTYEAYSHLLCYLRGL 120
DB 61 YLNYLGPPFPNEPDPNPPRLGAETLPRATVDLEWVRSNDKRLTQNTYEAYSHLLCYLRGL 120
QY 121 NRQAATAELRSLAHFCTSLQGLGSIAGVMAALGYPLPQPLGTEPTWTTPGPAHSDFLQ 180
DB 121 NRQAATAELRSLAHFCTSLQGLGSIAGVMAALGYPLPQPLGTEPTWTTPGPAHSDFLQ 180
QY 181 KMDDFWLLKELQTLWRSKDFNRLKKQPPAAAATLHLGAHGF 225
DB 181 KMDDFWLLKELQTLWRSKDFNRLKKQPPAAAATLHLGAHGF 225

RESULT 5
US-08-792-019B-5
; Sequence 5, Application US/08792019B
; Patent No. 5741772
; GENERAL INFORMATION:
; APPLICANT: CHANG, MING-SHI
; TITLE OF INVENTION: THE NEUROTROPHIC FACTOR NNT-1
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMGEN INC.
; STREET: 1840 DEHAVILLAND DRIVE
; CITY: THOUSAND OAKS
; STATE: CA
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/792,019B
; FILING DATE: 03-FEB-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
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```
; NAME: COOK, ROBERT R.
; REGISTRATION NUMBER: 31,602
; REFERENCE/DOCKET NUMBER: A-442
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 225 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-792-019B-5

Query Match 97.3%; Score 1193; DB 1; Length 225;
Best Local Similarity 96.9%; Pred. No. 1.4e-125;
Matches 218; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDLRAGDSWGLACICTVLWHLPAVPALNRTGDPGPGSIQKTYDLTRYLEHQLRSLAGT 60
DB 1 MDLRAGDSWGLACICTVLWHLPAVPALNRTGDPGPGSIQKTYDLTRYLEHQLRSLAGT 60
QY 61 YLNYLGPPFPNEPDPNPPRLGAETLPRATVDLEWVRSNDKRLTQNTYEAYSHLLCYLRGL 120
DB 61 YLNYLGPPFPNEPDPNPPRLGAETLPRATVDLEWVRSNDKRLTQNTYEAYSHLLCYLRGL 120
QY 121 NRQAATAELRSLAHFCTSLQGLGSIAGVMAALGYPLPQPLGTEPTWTTPGPAHSDFLQ 180
DB 121 NRQAATAELRSLAHFCTSLQGLGSIAGVMAALGYPLPQPLGTEPTWTTPGPAHSDFLQ 180
QY 181 KMDDFWLLKELQTLWRSKDFNRLKKQPPAAAATLHLGAHGF 225
DB 181 KMDDFWLLKELQTLWRSKDFNRLKKQPPAAAATLHLGAHGF 225
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RESULT 6
US-08-988-819-5
; Sequence 5, Application US/08988819
; Patent No. 6054294
; GENERAL INFORMATION:
; APPLICANT: CHANG, MING-SHI
; TITLE OF INVENTION: NEUROTROPHIC FACTOR NNT-1
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMGEN INC.
; STREET: ONE AMGEN CENTER DRIVE
; CITY: THOUSAND OAKS
; STATE: CA
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/988,819
; FILING DATE: 12-DEC-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/792,019
; FILING DATE: 03-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: COOK, ROBERT R.
; REGISTRATION NUMBER: 31,602
; REFERENCE/DOCKET NUMBER: A-442A
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 225 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-988-819-5

Query Match 97.3%; Score 1193; DB 3; Length 225;
Best Local Similarity 96.9%; Pred. No. 1.4e-125;
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Matches 218; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDLRAGDSWGLACCTVWLHLPVAVPALNRTGDPGPGPSIQKTYDILTRYLEHQRLSLAGT 60
DB 1 MDLRAGDSWGLACCTVWLHLPVAVPALNRTGDPGPGPSIQKTYDILTRYLEHQRLSLAGT 60
QY 61 YLYNLGPPFPNEPDPNPRGAEITLPRATVDLEWRSNDKRLTONYEAYSHLLCYLRLG 120
DB 61 YLYNLGPPFPNEPDPNPRGAEITLPRATVDLEWRSNDKRLTONYEAYSHLLCYLRLG 120
QY 121 NROQATAEIRSLAHFCTSLQGLGSIAGVMAALGYPLPOLPCTEPTWTPGPAHSDFLQ 180
DB 121 NROQATAEIRSLAHFCTSLQGLGSIAGVMAALGYPLPOLPCTEPTWTPGPAHSDFLQ 180
QY 181 KMDDFWLLKELQTLWRSKDFNRLKKKQMPAAAVTLHLGAHGF 225
DB 181 KMDDFWLLKELQTLWRSKDFNRLKKKQMPAAAVTLHLGAHGF 225

RESULT 7

US-09-016-534-5
; Sequence 5, Application US/09016534
; Patent No. 6143874
; GENERAL INFORMATION:
; APPLICANT: CHANG, MING-SHI
; APPLICANT: ELLIOTT, GARY S.
; APPLICANT: SARMIENTO, ULLA
; APPLICANT: SENALDI, GIORGIO
; TITLE OF INVENTION: THE NEUROTROPIC FACTOR NNT-1
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMGEN INC.
; STREET: ONE AMGEN CENTER
; CITY: THOUSAND OAKS
; STATE: CA
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,534
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/792,019
; FILING DATE: 03-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: COOK, ROBERT R.
; REGISTRATION NUMBER: 31,602
; REFERENCE/DOCKET NUMBER: A-442B
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 225 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-534-5

Query Match 97.3%; Score 1193; DB 3; Length 225;
Best Local Similarity 96.9%; Pred. No. 1.4e-125;
Matches 218; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDLRAGDSWGLACCTVWLHLPVAVPALNRTGDPGPGPSIQKTYDILTRYLEHQRLSLAGT 60
DB 1 MDLRAGDSWGLACCTVWLHLPVAVPALNRTGDPGPGPSIQKTYDILTRYLEHQRLSLAGT 60
QY 61 YLYNLGPPFPNEPDPNPRGAEITLPRATVDLEWRSNDKRLTONYEAYSHLLCYLRLG 120
DB 61 YLYNLGPPFPNEPDPNPRGAEITLPRATVDLEWRSNDKRLTONYEAYSHLLCYLRLG 120

QY 121 NROQATAEIRSLAHFCTSLQGLGSIAGVMAALGYPLPOLPCTEPTWTPGPAHSDFLQ 180
DB 121 NROQATAEIRSLAHFCTSLQGLGSIAGVMAALGYPLPOLPCTEPTWTPGPAHSDFLQ 180
QY 181 KMDDFWLLKELQTLWRSKDFNRLKKKQMPAAAVTLHLGAHGF 225
DB 181 KMDDFWLLKELQTLWRSKDFNRLKKKQMPAAAVTLHLGAHGF 225

RESULT 8

US-09-106-182-3
; Sequence 3, Application US/09106182
; Patent No. 6046035
; GENERAL INFORMATION:
; APPLICANT: Shi, Yangu
; APPLICANT: Ruben, Steve
; TITLE OF INVENTION: Cardiotrophin-Like Cytokine
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc
; STREET: 9410 Key West Ave
; CITY: Rockville
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/106,182
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/051,053
; FILING DATE: 30-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF385
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 203 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-106-182-3

Query Match 10.2%; Score 124.5; DB 3; Length 203;
Best Local Similarity 28.1%; Pred. No. 8e-06;
Matches 50; Conservative 24; Mismatches 85; Indels 19; Gaps 5;

QY 40 IQKTYDILTRYLEHQRLSLAGTLYNLGPPFPNEPDPNPRGAEITLPRATVDLEWRS 96
DB 27 IQKTYDILTRYLEHQRLSLAGTLYNLGPPFPNEPDPNPRGAEITLPRATVDLEWRS 93
QY 97 LNDKRLTONYEAYSHLLCYLRLGSLNROAA-----TAEIRSLAHFCTSLQGLGSIAGV 151
DB 84 ---SERLRQDAALSAIPALLDAVRRRQAEINPRAPRILRLSLDAAARQVRALGAAVETVL 140
QY 152 AALGY----PLPGLPCTEPTWTPGPAHSDFLQKMDDFWLLKELQTLWRSKDFNRL 205
DB 141 AALGAAAGFVPEV-ATSAFLTNSAAGVFAKVLGLHVGILYGEWVSRTEGDLGQL 197

RESULT 9

US-08-233-609-3
; Sequence 3, Application US/08233609

Patent No. 5534615
GENERAL INFORMATION:
APPLICANT: Baker, Joffre
APPLICANT: Chien, Kenneth
APPLICANT: King, Kathleen
APPLICANT: Pennica, Diane
APPLICANT: Wood, William
TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses Therefor
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,609
FILING DATE: 25-APR-1994
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER: 08/233609
FILING DATE: 25-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/286304
FILING DATE: 05-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 894P1DS
TELEPHONE: 415/225-8674
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 203 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-233-609-3
Query Match 9.7%; Score 118.5; DB 1; Length 203;
Best Local Similarity 28.8%; Pred. No. 3.8e-05;
Matches 51; Conservative 21; Mismatches 88; Indels 17; Gaps 5;
QY 40 IQKTYDLTRYLEHQRLSLAGTYLVNLYGPPFNEPDNPRL---GAETLPRATVDLEWRS 96
Db 27 IROTHNARLLTKYAEQLLEEVVQQGEPFGLPGFSPRLPLAGLSGPAPSHAGLPV--- 83
QY 97 LNDKRLTQNYEAYSHLLCYLRLGNRQA-----TAELRRLSLAHFCTSLQGLLSIAGVM 151
Db 84 ---SERLRQDAALSVLPALLDAVRRRQAEINPRAPRLRLSLDAAARQVRLGAATVTL 140
QY 152 AALGYPL--PQPLPGTEPT-WTEGPAHSDFLQKDDFWLLKELQTLWLSAKDFNRL 205
Db 141 AALGAARGPGPEVTVATLFTANSTAGIFS AKVLGFHVCGLYGEWVSRTEGDLQQL 197
RESULT 10
US-08-444-083-3
Sequence 3: Application US/08444083
Patent No. 5571675
GENERAL INFORMATION:
APPLICANT: Baker, Joffre
APPLICANT: Chien, Kenneth
APPLICANT: King, Kathleen
APPLICANT: Pennica, Diane
APPLICANT: Wood, William
TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses Therefor
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,609
FILING DATE: 25-APR-1994
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER: 08/233609
FILING DATE: 25-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/286304
FILING DATE: 05-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 894
TELEPHONE: 415/225-1896
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 203 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-233-609-3
Query Match 9.7%; Score 118.5; DB 1; Length 203;
Best Local Similarity 28.8%; Pred. No. 3.8e-05;
Matches 51; Conservative 21; Mismatches 88; Indels 17; Gaps 5;
QY 40 IQKTYDLTRYLEHQRLSLAGTYLVNLYGPPFNEPDNPRL---GAETLPRATVDLEWRS 96
Db 27 IROTHNARLLTKYAEQLLEEVVQQGEPFGLPGFSPRLPLAGLSGPAPSHAGLPV--- 83
QY 97 LNDKRLTQNYEAYSHLLCYLRLGNRQA-----TAELRRLSLAHFCTSLQGLLSIAGVM 151
Db 84 ---SERLRQDAALSVLPALLDAVRRRQAEINPRAPRLRLSLDAAARQVRLGAATVTL 140
QY 152 AALGYPL--PQPLPGTEPT-WTEGPAHSDFLQKDDFWLLKELQTLWLSAKDFNRL 205
Db 141 AALGAARGPGPEVTVATLFTANSTAGIFS AKVLGFHVCGLYGEWVSRTEGDLQQL 197
RESULT 10
US-08-444-083-3
Sequence 3: Application US/08444083
Patent No. 5571675
GENERAL INFORMATION:
APPLICANT: Baker, Joffre
APPLICANT: Chien, Kenneth
APPLICANT: King, Kathleen
APPLICANT: Pennica, Diane
APPLICANT: Wood, William
TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses Therefor
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,609
FILING DATE: 25-APR-1994
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER: 08/233609
FILING DATE: 25-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/286304
FILING DATE: 05-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 894
TELEPHONE: 415/225-1896
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 203 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-233-609-3
Query Match 9.7%; Score 118.5; DB 1; Length 203;
Best Local Similarity 28.8%; Pred. No. 3.8e-05;
Matches 51; Conservative 21; Mismatches 88; Indels 17; Gaps 5;
QY 40 IQKTYDLTRYLEHQRLSLAGTYLVNLYGPPFNEPDNPRL---GAETLPRATVDLEWRS 96
Db 27 IROTHNARLLTKYAEQLLEEVVQQGEPFGLPGFSPRLPLAGLSGPAPSHAGLPV--- 83
QY 97 LNDKRLTQNYEAYSHLLCYLRLGNRQA-----TAELRRLSLAHFCTSLQGLLSIAGVM 151
Db 84 ---SERLRQDAALSVLPALLDAVRRRQAEINPRAPRLRLSLDAAARQVRLGAATVTL 140
QY 152 AALGYPL--PQPLPGTEPT-WTEGPAHSDFLQKDDFWLLKELQTLWLSAKDFNRL 205
Db 141 AALGAARGPGPEVTVATLFTANSTAGIFS AKVLGFHVCGLYGEWVSRTEGDLQQL 197
RESULT 11
US-08-286-304-3
Sequence 3, Application US/08286304
Patent No. 5571893
GENERAL INFORMATION:
APPLICANT: Baker, Joffre
APPLICANT: Chien, Kenneth
APPLICANT: King, Kathleen
APPLICANT: Pennica, Diane
APPLICANT: Wood, William
TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses Therefor
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,083
FILING DATE: 17-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/233609
FILING DATE: 25-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/286304
FILING DATE: 05-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 894P1DS
TELEPHONE: 415/225-8674
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 203 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-444-083-3
Query Match 9.7%; Score 118.5; DB 1; Length 203;
Best Local Similarity 28.8%; Pred. No. 3.8e-05;
Matches 51; Conservative 21; Mismatches 88; Indels 17; Gaps 5;
QY 40 IQKTYDLTRYLEHQRLSLAGTYLVNLYGPPFNEPDNPRL---GAETLPRATVDLEWRS 96
Db 27 IROTHNARLLTKYAEQLLEEVVQQGEPFGLPGFSPRLPLAGLSGPAPSHAGLPV--- 83
QY 97 LNDKRLTQNYEAYSHLLCYLRLGNRQA-----TAELRRLSLAHFCTSLQGLLSIAGVM 151
Db 84 ---SERLRQDAALSVLPALLDAVRRRQAEINPRAPRLRLSLDAAARQVRLGAATVTL 140
QY 152 AALGYPL--PQPLPGTEPT-WTEGPAHSDFLQKDDFWLLKELQTLWLSAKDFNRL 205
Db 141 AALGAARGPGPEVTVATLFTANSTAGIFS AKVLGFHVCGLYGEWVSRTEGDLQQL 197
RESULT 11
US-08-286-304-3
Sequence 3, Application US/08286304
Patent No. 5571893
GENERAL INFORMATION:
APPLICANT: Baker, Joffre
APPLICANT: Chien, Kenneth
APPLICANT: King, Kathleen
APPLICANT: Pennica, Diane
APPLICANT: Wood, William
TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses Therefor
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:

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; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/286,304
; FILING DATE: 05-AUG-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/233609
; FILING DATE: 25-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 894P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 203 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-286-304-3

Query Match
Best Local Similarity 9.7%; Score 118.5; DB 1; Length 203;
Matches 51; Conservative 21; Mismatches 88; Indels 17; Gaps 5;

QY 40 IQKTYDLTRYLEHQLRSLAGTYLNYLGGPPFNEPDPNPRL--GAETLPRAATVDLEWVRS 96
Db 27 IRQTHNLARLLTKYAEQLLEEVYQQOGEPPGLGFGSPRLPLAGLSGAPAPSHAGLPV--- 83
QY 97 LNDKRLTQNYEAYSHLLCYLRGLNQAA-----TAE LRSLAHFCTSLQGLGSIAGVM 151
Db 84 ---SERLRQDAALSVLPALLDAVRRRQAEINPRAPRLRLSLEDAARQVRAALGAAVETVL 140
QY 152 AALGYPL--PQLPGCTEPT-WTPGPAHSDFLQKMDDFWLLKELQTLWRSKDFNRL 205
Db 141 AALGAARGPGPEPVTVAITFTANSTAGIFSAKVLGFHVCGLYGEWVSRTEGDLQQL 197

RESULT 12
US-08-442-745-3
; Sequence 3, Application US/08442745
; Patent No. 5624806
; GENERAL INFORMATION:
; APPLICANT: Baker, Joffre
; APPLICANT: Chien, Kenneth
; APPLICANT: King, Kathleen
; APPLICANT: Pennica, Diane
; APPLICANT: Wood, William
; TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses Therefor
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/442,745
; FILING DATE: 17-may-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/233609

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; FILING DATE: 25-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/286304
; FILING DATE: 05-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Torchia, Timothy E.
; REGISTRATION NUMBER: 36,700
; REFERENCE/DOCKET NUMBER: 894PID1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-8674
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 203 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-442-745-3

Query Match
Best Local Similarity 9.7%; Score 118.5; DB 1; Length 203;
Matches 51; Conservative 21; Mismatches 88; Indels 17; Gaps 5;

QY 40 IQKTYDLTRYLEHQLRSLAGTYLNYLGGPPFNEPDPNPRL--GAETLPRAATVDLEWVRS 96
Db 27 IRQTHNLARLLTKYAEQLLEEVYQQOGEPPGLGFGSPRLPLAGLSGAPAPSHAGLPV--- 83
QY 97 LNDKRLTQNYEAYSHLLCYLRGLNQAA-----TAE LRSLAHFCTSLQGLGSIAGVM 151
Db 84 ---SERLRQDAALSVLPALLDAVRRRQAEINPRAPRLRLSLEDAARQVRAALGAAVETVL 140
QY 152 AALGYPL--PQLPGCTEPT-WTPGPAHSDFLQKMDDFWLLKELQTLWRSKDFNRL 205
Db 141 AALGAARGPGPEPVTVAITFTANSTAGIFSAKVLGFHVCGLYGEWVSRTEGDLQQL 197

RESULT 13
US-08-443-129-3
; Sequence 3, Application US/08443129
; Patent No. 5627073
; GENERAL INFORMATION:
; APPLICANT: Baker, Joffre
; APPLICANT: Chien, Kenneth
; APPLICANT: King, Kathleen
; APPLICANT: Pennica, Diane
; APPLICANT: Wood, William
; TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses Therefor
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/443,129
; FILING DATE: 17-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/233609
; FILING DATE: 25-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/286
; FILING DATE: 05-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 304
; FILING DATE: (null)

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TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 203 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-443-952-3

Query Match          9.7%; Score 118.5; DB 1; Length 203;
Best Local Similarity 28.8%; Pred.No.3.8e-05;
Matches 51; Conservative 21; Mismatches 88; Indels 17; Gaps 5;

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Db      27 IRQTHTNLAELLTKYAQLLEEIVQQGGPGFGLPGFPSPPLPLAGLSGPAPSHAGLPV--- 83

QY      97 LNDKURLTQNVEAYSHLLCYLRGLNRQA-----TAELRSLAHFCTSLQGLLGSTAGVM 151
       | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      84 ---SERLRQRDAALSVLPALLIDAVRRQAEINPRAPRLRLSRLEDAAARQVRALGAAVETVL 140

QY      152 AALGYPL--POLPCTEPT-WTPGPAHSDFLQXMDDFLLKELQTLWLWSAKDFNL 205
       |||||   | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      141 AALGAAARGPGEPTVTALTFTANSTAGISAKVLGFHVCGLYGEWVSRTGDGLQL 197


RESULT 15
US-08-443-130-3
; Sequence 3, Application US/08443130
; Patent No. 5723585
; GENERAL INFORMATION:
; APPLICANT: Baker, Joffre
; APPLICANT: Chien, Kenneth
; APPLICANT: King, Kathleen
; APPLICANT: Pennica, Diane
; APPLICANT: Wood, William
; TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses
; TITLE OF INVENTION: Therefor
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/443,130
; FILING DATE: 17-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/233609
; FILING DATE: 25-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/286304
; FILING DATE: 05-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Torchia, Timothy E.
; REGISTRATION NUMBER: 36,700
; REFERENCE/DOCKET NUMBER: 894FLD3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-8674
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 203 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

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US-08-443-130-3

Query Match	9.7%	Score 118.5	DB 1	Length 203
Best Local Similarity	28.8%	Pred. No. 3.8e-05		
Matches	51	Conservative	21	Mismatches 88
		Indels	17	Gaps 5

QY	40	IQKTYDLTRYLEHQRLSLAGTYLNLYLGGPPFNEPDPFNPPRL---GAETLPRATVDLEVWRS	96
DB	27	IRQTHNLARLLTKYAEQLLEEYVQQQGEFFGLPGFSPPLPLAGLSGPAPSHAGLPV---	83
QY	97	LNDKRLTQNYEAYSHLLCYLRGLNRQAA-----TAE LRSLAHFCTSLQGLLSGIAGVM	151
DB	84	---SESLRQDAALSVLPALLDAVRERQAE LNFRAPRLRLRSLEDAARQVRALGAAVETVL	140
QY	152	AALGYPL--PQPLPGTEPT-WTEGPAHSDFLOKMDDFWLLKELQTLWRSKDFNRL	205
DB	141	AALGAAARGPEPVTATLFTANSTAGIFS AKVLGFHVCGLYGEWVSRTGDLGQL	197

Search completed: August 10, 2004, 06:48:27
Job time : 17 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 15, 2004, 12:20:54 ; Search time 19013.8 Seconds
(without alignments)
11596.087 Million cell updates/sec

Title: US-09-931-704-3

Perfect score: 5087

Sequence: 1 aacctgcgagtgggcctggc.....cctttgctaagtcttcctca 5087

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 s

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3: gb_in:*
4: gb_om:*
5: gb_ov:*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	Score	Match	Length		
1	5087	100.0	5087	6	AR002596 Sequence
2	5087	100.0	5087	6	AX392088 Sequence
3	5087	100.0	5087	6	BD195448 The neuro
4	5087	100.0	5087	9	AF176912 Homo sapi
5	4910.8	96.5	168565	9	AP003419 Homo sapi
6	4908.8	96.5	169144	2	AC005849 Homo sapi
7	4605	90.5	135116	2	AF002437 Homo sapi
8	1709.4	33.6	246093	2	AC140073 Mus muscu
9	1709.4	33.6	269155	10	AC109138 Mus muscu
10	1632.6	32.1	258710	2	AC135823 Rattus no
11	1463.4	28.8	1710	6	BD132824 Cardiotro
12	1463.4	28.8	1736	9	BC012939 Homo sapi
13	1461.4	28.7	1689	9	AF172854 Homo sapi
14	525.4	10.3	881	6	AX205024 Sequence
15	525.4	10.3	881	6	AX205042 Sequence
16	523.4	10.3	797	6	AR002595 Sequence
17	523.4	10.3	797	6	AX392086 Sequence
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19	523.4	10.3	797	9	AF176911 Homo sapi
20	495.4	9.7	680	9	AY049779 Homo sapi
21	492.8	8.7	1692	6	AX205060 Sequence
22	429.6	8.4	819	6	AR002597 Sequence
23	429.6	8.4	819	6	AX392089 Sequence
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27	329	6.5	340	6	AX903004 Sequence
28	329	6.5	340	6	BD038537 Sequence
29	324.6	6.4	396	6	BD132825 Cardiotro
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31	148.8	2.9	6347	2	AC110526 Mus muscu
32	99	1.9	7218	6	166494 Sequence 14
33	82.8	1.6	179145	9	AC009785 Homo sapi
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36	78	1.5	254982	2	AC102125 Mus muscu
37	74.8	1.5	233361	2	BX510356 Danio rer
38	74.2	1.5	254967	2	AC112091 Rattus no
39	73.8	1.5	203982	9	AC067854 Homo sapi
40	73.2	1.4	168873	2	BX324816 Danio rer
41	73.2	1.4	195690	10	AC098726 Mus muscu
42	72.2	1.4	99419	2	AC140090 Ornithoth
43	72.2	1.4	120874	2	AC139116 Ornithoth
44	70.6	1.4	95097	9	AL133232 Human DNA
45	70.6	1.4	163515	2	AC144753 Ornithoth

ALIGNMENTS

RESULT 1
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 LOCUS
 DEFINITION
 SEQUENCE 3 from patent US 5741772.
 AR002596
 ACCESSION
 AR002596.1 GI:3964150
 VERSION
 KEYWORDS
 .
 UNKNOWN.
 SOURCE
 ORGANISM
 UNCLASSIFIED.
 REFERENCE
 1 (bases 1 to 5087)
 AUTHORS
 Chang, M.-s.
 TITLE
 Neurotrophic factor NNT-1
 JOURNAL
 Patent: US 5741772-A 3 21-APR-1998;
 FEATURES
 Location/Qualifiers

source	1...5087	/organism="unknown"	/mol_type="unassigned DNA"
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Best Local Similarity	100.0%;	Pred. No. 0;	
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QY	61	CTCCACTCCGACGCTTCGGAGAGCGCGACCGCGCGCGCGCGCGCGCGCGCA	120
DB	61	CTCCACTCCGACGCTTCGGAGAGCGCGACCGCGCGCGCGCGCGCGCGCGCA	120
QY	121	TGGACCTCCGAGCAGGTTGAAACCCAACTAGCCCTGCTTTCATATACATGACAAGCAG	180
DB	121	TGGACCTCCGAGCAGGTTGAAACCCAACTAGCCCTGCTTTCATATACATGACAAGCAG	180
QY	181	CGCCCATCTGATACCTAAACCGACCAAGTACAGCCCTCCAACTCACGCTTGCCTGCC	240
DB	181	CGCCCATCTGATACCTAAACCGACCAAGTACAGCCCTCCAACTCACGCTTGCCTGCC	240
QY	241	CAGACCTCACCACATCTTGTGACTCAAACTCAACCGCACTAAATCAACCAATCCCA	300
DB	241	CAGACCTCACCACATCTTGTGACTCAAACTCAACCGCACTAAATCAACCAATCCCA	300
QY	301	AGCTAAACTATCTGAACCTTTTAAAGTAACCCAGTCTTAACTCAACCTAGCCCAAT	360
DB	301	AGCTAAACTATCTGAACCTTTTAAAGTAACCCAGTCTTAACTCAACCTAGCCCAAT	360
QY	361	GCAATATATCTACCTAGCAACCCCTAAGTCTTGGCAGTCCAAAGTGTCCACTG	420
DB	361	GCAATATATCTACCTAGCAACCCCTAAGTCTTGGCAGTCCAAAGTGTCCACTG	420
QY	421	AATCCTCAGCTTGGTCTCACTGAAATCCAGAAAGCAATATTTCCCACTGCCCCAT	480
DB	421	AATCCTCAGCTTGGTCTCACTGAAATCCAGAAAGCAATATTTCCCACTGCCCCAT	480
QY	481	CCCTCTTACAGCACCAACCTGGCTGCTGACTCTGGTATCTCTGGATGTCCAACT	540
DB	481	CCCTCTTACAGCACCAACCTGGCTGCTGACTCTGGTATCTCTGGATGTCCAACT	540
QY	541	CTGAGTGCCATCAGCAACCAAGCCGACTCTGCAAAATGCACCTCTCTCCCTTCCGTCC	600
DB	541	CTGAGTGCCATCAGCAACCAAGCCGACTCTGCAAAATGCACCTCTCTCCCTTCCGTCC	600
QY	601	CAACCTTGAGGCTGATGAAAGGCTCATTTGAAGTCCAACTTTTCCCACTAACACC	660
DB	601	CAACCTTGAGGCTGATGAAAGGCTCATTTGAAGTCCAACTTTTCCCACTAACACC	660
QY	661	AAGAACGGGTGAACCTCCACACTGCCACCGTTCCTGAGAGTGAGCACTAAATCTCCTT	720
DB	661	AAGAACGGGTGAACCTCCACACTGCCACCGTTCCTGAGAGTGAGCACTAAATCTCCTT	720
QY	721	CAATTAACCCCACTACATTTCCACACTCAGGAATCACATCTAGTAATATACCCAA	780
DB	721	CAATTAACCCCACTACATTTCCACACTCAGGAATCACATCTAGTAATATACCCAA	780
QY	781	ACTAAGCCCATAGGAGCGCGGACCTAGTGTCTAAGCCCTATACCTTGTCTCTATGG	840
DB	781	ACTAAGCCCATAGGAGCGCGGACCTAGTGTCTAAGCCCTATACCTTGTCTCTATGG	840
QY	841	GTGAGTCTGTCTTGGCGGCGGCTCTCTCTCTGCTTCTCTCTCTCTCTCTCTCTCT	900
DB	841	GTGAGTCTGTCTTGGCGGCGGCTCTCTCTCTGCTTCTCTCTCTCTCTCTCTCTCT	900
QY	901	AGCTGCGACTGTGACATGTCTCTCCACCTCTGACTCCCTCAAGCTGCAAGTGG	960
DB	901	AGCTGCGACTGTGACATGTCTCTCCACCTCTGACTCCCTCAAGCTGCAAGTGG	960
QY	961	GACTGGAAGACTGGCAGGAAGCTAGGGTACAACTGGAAACACAGGAGGTGCACTGCACT	1020
DB	961	GACTGGAAGACTGGCAGGAAGCTAGGGTACAACTGGAAACACAGGAGGTGCACTGCACT	1020
QY	1021	CCCTAGGCTGGCCCGCTCCCTCCATGTACACATATACATGTGGCACACACACAGTG	1080
DB	1021	CCCTAGGCTGGCCCGCTCCCTCCATGTACACATATACATGTGGCACACACACAGTG	1080
QY	1081	GCACATATCCAAAGACTCTCTCAGCTGACACACAGATCCATTCTCAAGTATCTACTGAT	1140
DB	1081	GCACATATCCAAAGACTCTCTCAGCTGACACACAGATCCATTCTCAAGTATCTACTGAT	1140
QY	1141	AGACACTCATGTGTCGAAGTCTCTCATCTCAAAATACACATGCTCTCTCTCTCTCC	1200
DB	1141	AGACACTCATGTGTCGAAGTCTCTCATCTCAAAATACACATGCTCTCTCTCTCTCC	1200
QY	1201	GTCTTGGCAGAGTGTTCCTCTCCATCCCTCTCCATCTCCATCTCTCTCTCTCTCTCT	1260
DB	1201	GTCTTGGCAGAGTGTTCCTCTCCATCCCTCTCCATCTCCATCTCTCTCTCTCTCT	1260
QY	1261	TCACCCCTCCACAGCCCAAGGTGGGACAGACACCTGAGGGGCTGCCAGCTGCTTCC	1320
DB	1261	TCACCCCTCCACAGCCCAAGGTGGGACAGACACCTGAGGGGCTGCCAGCTGCTTCC	1320
QY	1321	GTGTGGGCTCGGCGCGGCTCATGCTTCTGTCCATCTCTGCCACAGGGGACTCGTGGG	1380
DB	1321	GTGTGGGCTCGGCGCGGCTCATGCTTCTGTCCATCTCTGCCACAGGGGACTCGTGGG	1380
QY	1381	GATGTTAGCTGCTGTGCACGGTGTCTGTGGACCTCTCCCTGAGTGCCAGCTCTCAATCG	1440
DB	1381	GATGTTAGCTGCTGTGCACGGTGTCTGTGGACCTCTCCCTGAGTGCCAGCTCTCAATCG	1440
QY	1441	CACAGGGACCCAGGGCTTGGCCCTCCATCCAGAAAACCTATGACTCACCGGTACTCT	1500
DB	1441	CACAGGGACCCAGGGCTTGGCCCTCCATCCAGAAAACCTATGACTCACCGGTACTCT	1500
QY	1501	GGAGCACTACTCCGAGCTTGGCTGGGACCTATGTAGTATCCAGCTAGGAATCTGGG	1560
DB	1501	GGAGCACTACTCCGAGCTTGGCTGGGACCTATGTAGTATCCAGCTAGGAATCTGGG	1560
QY	1561	AGTTGGGGAGGAGTGGAGGTTGGGAAAAGACAGTCTTAACCTGGAGGGTCTGGTAA	1620
DB	1561	AGTTGGGGAGGAGTGGAGGTTGGGAAAAGACAGTCTTAACCTGGAGGGTCTGGTAA	1620
QY	1621	TGATGGGCTGAGGAGGGCTTGTGCTCCACAGTCCCTCTGTCTGTGTCTATCTCTG	1680
DB	1621	TGATGGGCTGAGGAGGGCTTGTGCTCCACAGTCCCTCTGTCTGTGTCTATCTCTG	1680
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QY	1801	TCCCTCTGGGGGCGGGGAAAGTCTCTCTGTGTTTACACCGTGTGTGTGTGTGTGT	1860
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QY	1861	GGCGGGTGTGGGTGGGAGACAGAGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	1920
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QY	1921	TGCCCCCAGACCTGGGCGCTGTGTCTGGAACCCAGGGGCTCCCTTCCGTCTGCTCT	1980
DB	1921	TGCCCCCAGACCTGGGCGCTGTGTCTGGAACCCAGGGGCTCCCTTCCGTCTGCTCT	1980
QY	1981	CCCATCTAGCTGGGCTCTCTAGGGGGTCTATGGGGGAGGGGACTGTAGGGAGCCAGG	2040
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QY	2041	CAGTAGTGGCAGGGGTTTAGGGTGTGATGGAGTTATGCTGTAGGATTTAGGGGTGG	2100

Db 2041 CAGTAGTGGCAGGGGTTTAGGGTGTGGATGGAGGTTATGCTGAAGATTGGGGTGG 2100
Qy 2101 TCCAGAGGTGTTTCCAGAGCCCGAGAGAGAGAGAGAGAGAGGTTTGGAGAGCCGAGGACCC 2160
Db 2101 TCCAGAGGTGTTTCCAGAGCCCGAGAGAGAGAGAGAGAGGTTTGGAGAGCCGAGGACCC 2160
Qy 2161 ATGGGGAACCGGCCCTCTTCCCGTGTCTCTCTTCCACATCCAGACCCCTACTCTGGAG 2220
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Qy 2221 CCAGGGAAGAAAAGGGAAGAGTGGCGGGGAGCTGGCTCCAGCCCGCAGATACACCG 2280
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VERSION BD195448.1 GI:33005218
KEYWORDS JP 2002514067-A/2.
SOURCE unidentified
ORGANISM unidentified

BD195448 5087 bp DNA linear PAT 17-JUL-2003

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unclassified.
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AF176912
LOCUS

DEFINITION Homo sapiens neurotrophin-1/B-cell stimulating factor-3 gene,
complete cds.

ACCESSION AF176912

VERSION AF176912.1 GI:6007642

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

Senaldi,G., Varnum,B.C., Sarmiento,U., Starnes,C., Lile,J.,
Scully,S., Guo,J., Elliott,G., McNinch,J., Shaklee,C.L.,
Freeman,D., Manu,F., Simonet,W.S., Boone,T. and Chang,M.S.

Novel neurotrophin-1/B cell-stimulating factor-3: a cytokine of the
IL-6 family

Proc. Natl. Acad. Sci. U.S.A. 96 (20), 11458-11463 (1999)

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

Source

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Location/Qualifiers

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 REFERENCE 1
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 TITLE Homo sapiens genomic DNA
 JOURNAL Published Only in Database (2001)
 REFERENCE 2 (bases 1 to 168565)
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 TITLE Direct Submission
 JOURNAL Submitted (16-MAR-2001) Mashira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC), 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: hattori@gsc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/, Tel: 81-45-503-9111, Fax: 81-45-503-9170)
 COMMENT On Jun 16, 2003 this sequence version replaced gi:22202828.
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Db 47347 TCAGAGAGCCAGAGAGAGAGAGAGGGGTGTGAGGAGCGGAGG-ACCATGGGGAACCG 47289
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44408 GGTTCCTCCACCCACCTTTGCTTAAGTCTTCTCA 44373 Db
RESULT 6
AC005849/c
LOCUS AC005849 169144 bp DNA linear HTG 30-AUG-2001
DEFINITION Homo sapiens chromosome 11 clone CIT-HSP-1337H24, 9 unordered pieces.
ACCESSION AC005849
VERSION AC005849.1 GI:3779013
KEYWORDS HTG; HTGS PHASE1; HTGS_CANCELLED.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 169144)
Smith, D.R.
TITLE Sequencing of Human Chromosome 10
JOURNAL Unpublished
AUTHORS
REFERENCE 2 (bases 1 to 169144)
Smith, D.R.
JOURNAL Direct Submission
Submitted (22-OCT-1998) Genome Therapeutics Corporation, 100 Beaver Street, Waltham, MA 02154, USA
* NOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence. * as soon as it is available and the accession number will be preserved.
* 1 506: contig of 506 bp in length
* gap of unknown length
* *

*	507	3033:	contig	of 2527 bp in length
*			gap of	unknown length
*	3034	12956:	contig	of 9923 bp in length
*			gap of	unknown length
*	12957	19521:	contig	of 5565 bp in length
*			gap of	unknown length
*	19522	31636:	contig	of 12115 bp in length
*			gap of	unknown length
*	31637	48670:	contig	of 17034 bp in length
*			gap of	unknown length
*	48671	61610:	contig	of 12940 bp in length
*			gap of	unknown length
*	61611	97329:	contig	of 35719 bp in length
*			gap of	unknown length
*	97330	169144:	contig	of 71815 bp in length

ORIGIN

Query Match	96.5%;	Score 4908.8;	DB 2;	Length 169144;
Best Local Similarity	99.8%;	Pred. No. 0;		
Matches 4946;	Conservative	0;	Mismatches 7;	Indels 3; Gaps 3;
QY	133	CAGGTTGAACCCAAACTAGCCCTGCTCTT	CATAATGACAGACGCGCCCATCTGA	192
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QY	193	TACCTAAACCGACCAAGTACAGCGCCT	CCAACTCACCTCTGCTGCCAGACCTCACCA	252
Db	147120	TACCTAAACCGACCAAGTACAGCGCCT	CCAACTCACCTCTGCTGCCAGACCTCACCA	147061
QY	253	CATCTCTG-TGAGCTCAAACTCAACCGCA	CTAAATCAACCAATCCCAAGTCTTAACTA	311
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QY	312	ATCTGAAACTTTTAAAGTAAACCGAGT	CCCTTAAACCTAACCTAGCCCAATCCCAATTATAT	371
Db	147000	ATCTGAAACTTTTAAAGTAAACCGAGT	CCCTTAAACCTAACCTAGCCCAATCCCAATTATAT	146941
QY	372	CTACCTTAGCCAAACCCCTAACTGCTTT	GGCAGTCCAAAGTGCCACTGAATCCTCACCT	431
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QY	432	TGCTCTCTCACTGAAATCCGAGAAAG	CATATTTCCCACTGGCCCATCCCTCCCTTACA	491
Db	146880	TGCTCTCTCACTTAAATCCGAGAAAG	CATATTTCCCACTGGCCCATCCCTCCCTTACA	146821
QY	492	GCACCCACCCCTGGCCTCTGGACTCCT	GGTATCTCTGGGATGTCCAACTCTGCAGTGCCA	551
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QY	612	GSCTGATGGAAGGGCTCATTTGAAGT	CCAACTTTCCCACTTAAACACCAAGAACGGGT	671
Db	146700	GSCTGATGGAAGGGCTCATTTGAAGT	CCAACTTTCCCACTTAAACACCAAGAACGGGT	146641
QY	672	GAACTTCCACTGCGCACCGTTCCCT	GAGAGTGAGCACTAAATCTCCTTCAATCTTAACC	731
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QY	732	CACCTTACATTTCCACACTCAGGAAT	TCACATCTTAGATATACCCAAAATTAAGCCCCA	791
Db	146580	CACCTTACATTTCCACACTCAGGAAT	TCACATCTTAGATATACCCAAAATTAAGCCCCA	146521
QY	792	TAAAGCAGGCCGACCCCTAGTGTCT	TAAACCCCTATACCTTGTCTTCTATGGGTGAGTCTGT	851

Db	145441	GTGGGACAGAGGGGCCCACTCCATGCGTGGTTCCAGTCTGCCTCTGCCCCCAGAC	145388
Qy	1932	CTGGGGCCCTCTGCTCTGGAGCCAGGGGCGTCCTCTTCCGTCCTGCTCTCCCATCTAGC	1991
Db	145381	CTGGGGCCCTCTGCTCTGGAGCCAGGGGCGTCCTCTTCCGTCCTGCTCTCCCATCTAGC	145322
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Db	145321	TGGGCTCTCTTAGGGGGGTCA7TGGGGGAAGGGACTTAGGGAAACCCAGGCACTAGTGCA	145262
Qy	2052	GGGGGTTTAGGCTGTGAGTGAAGTATGCTGTAAAGATTGGGGGTGGTTCAGAGGGT	2111
Db	145261	GGGGGTTTAGGCTGTGGATGGAGGTTATGCTGTAAAGATTGGGGGTGGTTCAGAGGGT	145202
Qy	2112	TCAGAGCCCAAGGAGAGAAAGAGGAGGTGGAGAGCCGAGGACCAATGGGNAACG	2171
Db	145201	TCAGAGCCCAAGGAGAGAAAGAGGAGGTGGAGAGCCGAGGACCAATGGGNAACG	145143
Qy	2172	GGCCCTCTTCCGCTTCTCTTCCACATCCAGAGCCCTACTCTGGAGCCAGGGAAGA	2231
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Db	145082	AAAGGAGAGGGTGGCGGGGAGCTGGCTCCAGCCCAAGATACACCGAGGAATTAGT	145023
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Db	145022	TGTGCTCTGTGTTCTGACGCTGTGAACCTCCGCTGGGGCCCTGGCTATCCAGGSCCTC	144963
Qy	2352	TCCCTTGCTTCTCCCTTCTTCCAGATTATACATCTCCCTCATCCCTTCCCTGGGCC	2411
Db	14962	TCCCTTGCTTCTCCCTTCTTCCAGATTATACATCTCCCTCATCCCTTCCCTGGGCC	14903
Qy	2412	CAGCGCTCCCCGAGGTTGGAAAGGCTCTGGCTTCTCCCTATACATGCTGCTCTC	2471
Db	14902	CAGCGCTCCCCGAGGTTGGAAAGGCTCTGGCTTCTCCCTATACATGCTGCTCTC	14843
Qy	2472	CATAGCTTCTCTCTGCTCTACTCATAGAGCTGCTCCATTTCTTCTCTGCAACCCTG	2531
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Qy	2652	TCACTCTCTCTTGTTCCTGTGCAAGAAAACCTTGTGTTTCACTCCACTGCGCTCTCTAGT	2711
Db	144662	TCACTCTCTCTTGTTCCTGTGCAAGAAAACCTTGTGTTTCACTCCACTGCGCTCTCTAGT	144603
Qy	2712	TCCCGACCTTTTCTCTCTGGCTTCTCCCTGCCAAATTTCTCCAGAGTGCTCTACAC	2771
Db	144602	TCCCGACCTTTTCTCTCTGGCTTCTCCCTGCCAAATTTCTCCAGAGTGCTCTACAC	144543
Qy	2772	CCTCTGCTCCACTCTCTCCACCACTCACTCTTTAAACCCCTGCAATCTGGCTTCA	2831
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Qy	2892	TTTGAAGGCTCAATCTCTCTTGTGTCTTTTGAGGCCACACTGCTGAGGCTCTGCTCT	2951
Db	144422	TTTGAAGGCTCAATCTCTCTTGTGTCTTTTGAGGCCACACTGCTGAGGCTCTGCTCT	144363
Qy	2952	TCTCGAATCTCTCTCTTGGTCTCTGCACTCTCTTGGGCCACCTTCTACTCTCCAGCT	3011
Db	144362	TCTCGAATCTCTCTCTTGGTCTCTGCACTCTCTTGGGCCACCTTCTACTCTCCAGCT	144303

QY	3012	CCTCAGGCTCCTCTTCTCTCTGTCTGGCCCCACACGCGGGCACTCTCCAGGTTTCG	3071
DB	144302	CCTCAGGCTCCTCTTCTCTCTGTCTGGCCCCACACGCGGGCACTCTCCCAGGTTTCG	144243
QY	3072	CCACCAGCCAATCAGCACGTCCTTCTTGAGCGTCTTGCGTCTTCCTCCTCCTCTTTT	3131
DB	144242	CCACCAGCCAATCAGCACGTCCTTCTTGAGCGTCTTGCGTCTTCCTCCTCCTCTTT	144183
QY	3132	TCTAGGCCTCTCAATTGGAGAGCTCACACGCCACTGCTTCAACTGTACACTGATACA	3191
DB	144182	TCTAGGCCTCTCAATTGGAGAGCTCACACGCCACTGCTTCAACTGTACACTGATACA	144123
QY	3192	AATGATATCCTTAATTGGAAAAAATCAGGAGGCCATGAACAAAGAAGCCTAGCTGGAGA	3251
DB	144122	AATGATATCCTTAATTGGAAAAAATCAGGAGGCCATGAACAAAGAAGCCTAGCTGGAGA	144063
QY	3252	CAGGGCAGTGTCAAGGAGCACHAAAATAAGAACTTTGGGACAGGTATCTCTTGGTG	3311
DB	144062	CAGGGCAGTGTCAAGGAGCACHAAAATAAGAACTTTGGGACAGGTATCTCTTGGTG	144003
QY	3312	GTGAGCCAGCGGCTCTGCCCTCCTCCTTCCCATCACCCCTCTCTTTTCAACAGCTGAAT	3371
DB	144002	GTGAGCCAGCGGCTCTGCCCTCCTCCTTCCCATCACCCCTCTCTTTTCAACAGCTGAAT	143943
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DB	143942	ACCTGGGCCCCCTTTCAAAGCCAGACTTCAACCTCCCGCTCGGGGACAGACTC	143883
QY	3432	TGCCCAGGGCCACTGTTGACTTGGAGGTGTGGCGAAGCCTCAATGACAAACTGCGGCTGA	3491
DB	143882	TGCCCAGGGCCACTGTTGACTTGGAGGTGTGGCGAAGCCTCAATGACAAACTGCGGCTGA	143823
QY	3492	CCAGAACTAGAGGCTCAAGCCACCTTCTGTGTTACTTGGCTGSCCTCAACCGTCAGG	3551
DB	143822	CCAGAACTAGAGGCTCAAGCCACCTTCTGTGTTACTTGGCTGSCCTCAACCGTCAGG	143763
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DB	143762	CTGCCACTGTCTGAGCTGGCGCGCAGCCTGGCCCACTTCTGCAACAGCTTCCAGGCGCTCG	143703
QY	3612	TGGGACGATTTGGGGGCTCATGGCAGCTCTGGGCTACOCCTGCCACAGCGCTGCCGTG	3671
DB	143702	TGGGACGATTTGGGGGCTCATGGCAGCTCTGGGCTACOCCTGCCACAGCGCTGCCGTG	143643
QY	3672	GGACTGAACCCACTTGGACTCTTGCCCTTGCCCCACAGTAGCTTCTCTCAGAAAGATGGACG	3731
DB	143642	GGACTGAACCCACTTGGACTCTTGCCCTTGCCCCACAGTAGCTTCTCTCAGAAAGATGGACG	143583
QY	3732	ACTTCTGCTGCTGAAGAGCTGCAGACTGCTGTGGCGCTCGGCCAACAGGACTTCAACC	3791
DB	143582	ACTTCTGCTGCTGAAGAGCTGCAGACTGCTGTGGCGCTCGGCCAACAGGACTTCAACC	143523
QY	3792	GGCTCAAGAAGAATGAGCCTCCAGCAGCTGAGTCAACCTGCACCTTGGGGGCTCATG	3851
DB	143522	GGCTCAAGAAGAATGAGCCTCCAGCAGCTGAGTCAACCTGCACCTTGGGGGCTCATG	143463
QY	3852	GCTTCTGACTTCTGACCTTCTCTCTGCTCCCTCCCTTCAAACCTCTGCCACTTTGTG	3911
DB	143462	GCTTCTGACTTCTGACCTTCTCTCTGCTCCCTCCCTTCAAACCTCTGCCACTTTGTG	143403
QY	3912	AGAGCCAGCCTGTATGCCAAACCTGTTGAGCCAGGAGACAGAGCTGTGAGCCTCTGG	3971
DB	143402	AGAGCCAGCCTGTATGCCAAACCTGTTGAGCCAGGAGACAGAGCTGTGAGCCTCTGG	143343
QY	3972	CCCTTCTCTGACCGCTGGGCGTGTGATGCCAICAGCCCTGTCTCTCTCCCACTTCCCA	4031
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DB	143282	AAGGCTACCGAGCTGGGAGAGGTACAGTAGGCCCTGTCTGTCTCTGTTCTACAGGA	143223

QY 4092 AGTCATGCTCGAGGAGTGTGAAGTGGTTCAGTTGGTGCAGAGCGCTCATGGCTCCT 4151
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Db |||||
QY 4332 AAACAAACATGGTGGCAATTCACACAAAAGAGATGATTAACAGTGCAGGTTGGGG 4391
Db |||||
QY 142982 AAACAAACATGGTGGCAATTCACACAAAAGAGATGATTAACAGTGCAGGTTGGGG 142923
Db |||||
QY 4392 TCTGATTTGGAGGTGCCCTATAAACCAAGAGAAATACCTGAAGCACAGGGGACAGGA 4451
Db |||||
QY 142922 TCTGATTTGGAGGTGCCCTATAAACCAAGAGAAATACCTGAAGCACAGGGGACAGGA 142863
Db |||||
QY 4452 CAGACCAAGACAGACCCAGGAGTCTCCAAAGCACAGAGTGGCAACAAACCCGAGCTGA 4511
Db |||||
QY 142862 CAGACCAAGACAGACCCAGGAGTCTCCAAAGCACAGAGTGGCAACAAACCCGAGCTGA 142803
Db |||||
QY 4512 GCATCAGACCTTGCCTCGAATTCCTTCAGTATTAAGTGGCTCTTCTGCCCCCTT 4571
Db |||||
QY 142802 GCATCAGACCTTGCCTCGAATTCCTTCAGTATTAAGTGGCTCTTCTGCCCCCTT 142743
Db |||||
QY 4572 TCCAGGATATCTGTGGGTTCGCCAGGTGGGGAGGCAACCATAGCCACACACAGGATT 4631
Db |||||
QY 142742 TCCAGGATATCTGTGGGTTCGCCAGGTGGGGAGGCAACCATAGCCACACACAGGATT 142683
Db |||||
QY 4632 TCCTGAAAGTTACAAAGTACGATAGCATTTTGGGGTGAAGTGGCGACCTCCCAAGGCC 4691
Db |||||
QY 142682 TCCTGAAAGTTACAAAGTACGATAGCATTTTGGGGTGAAGTGGCGACCTCCCAAGGCC 142623
Db |||||
QY 4692 TGCCCCCAGCCACCCACCTGACTCTAAGTGTGTGTTAATTAATTTATTTT 4751
Db |||||
QY 142622 TGCCCCCAGCCACCCACCTGACTCTAAGTGTGTGTTAATTAATTTATTTT 142563
Db |||||
QY 4752 GAGATGTTATTTAGATGATTTATTTGAGAAATTTCTTCTGTTATTAACAATAA 4811
Db |||||
QY 142562 GAGATGTTATTTAGATGATTTATTTGAGAAATTTCTTCTGTTATTAACAATAA 142503
Db |||||
QY 4812 AATGCTTGCACCAAGACTTGTCTCTTGGCCAGCTCACCCCTCTGGTGTCTATCAGA 4871
Db |||||
QY 142502 AATGCTTGCACCAAGACTTGTCTCTTGGCCAGCTCACCCCTCTGGTGTCTATCAGA 142443
Db |||||
QY 4872 CTCTTGCACCCCTGGCTCCCACTTCCCTGTGCTGTGGAGCTGCACAGAGCTCTG 4931
Db |||||
QY 142442 CTCTTGCACCCCTGGCTCCCACTTCCCTGTGCTGTGGAGCTGCACAGAGCTCTG 142393
Db |||||
QY 4932 GGAAGAGCCCTCTTCTCCCGGACCTGGGGGAGTGGGCGACCTCAGACTTACCCACTG 4991
Db |||||
QY 142382 GGAAGAGCCCTCTTCTCCCGGACCTGGGGGAGTGGGCGACCTCAGACTTACCCACTG 142323
Db |||||
QY 4992 CTGCTGCGACCAACCAACCCCTTGATCTCCTCAGTCTCCCAACAGCTTCTGTCACCCCA 5051
Db |||||
QY 142322 CTGCTGCGACCAACCAACCCCTTGATCTCCTCAGTCTCCCAACAGCTTCTGTCACCCCA 142263
Db |||||
QY 5052 GGTTTCCCTCACCCCACTTGTGCTTGAAGTCTTCCTCA 5087
Db |||||
QY 142262 GGTTTCCCTCACCCCACTTGTGCTTGAAGTCTTCCTCA 142227
Db |||||

RESULT 7

AP002437

LOCUS

DEFINITION Homo sapiens chromosome 11 clone RP11-678D20 map 11q13, WORKING

135116 bp DNA linear

HTG 06-JUN-2000

DRAFT SEQUENCE, 41 unordered pieces.

AF002437
AP002437.1 GI:8307741
HTG: HTGS PHASE1: HTGS_DRAFT.
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 135116)
Hattori.M., Ishii.K., Toyoda.A., Taylor.T.D., Hong-Seog.P., Fujiyama.A., Yada.T., Totoki.Y., Watanabe.H. and Sakaki.Y.
Homo sapiens 135116 genomic DNA of 11q13
Published only in DataBase (2000)
2 (bases 1 to 135116)
Hattori.M., Ishii.K., Toyoda.A., Taylor.T.D., Hong-Seog.P., Fujiyama.A., Yada.T., Totoki.Y., Watanabe.H. and Sakaki.Y.
Direct Submission
Submitted (02-JUN-2000) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923, Fax:81-42-778-9924)
----- Genome Center
Center: RIKEN Genomic Sciences Center(GSC)
Center code: RIKEN
Web site: http://hgp.gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp
----- Project Information
Center project name: HumDraft11
Center clone name: RP11-678D20
----- Summary Statistics
Sequencing vector: PCR products; 100% of reads
Chemistry: Dye-terminator ET-amersham; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 109313 bases at least Q40
Consensus quality: 121923 bases at least Q30
Consensus quality: 127981 bases at least Q20
Insert size: 131116; sum-of-contigs
Quality coverage: 4.18x in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently consists of 41 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved

1 7749 contig of 7749 bp in length
7850 15108 contig of 7259 bp in length
15209 23728 contig of 8520 bp in length
23829 29302 contig of 5474 bp in length
29403 36171 contig of 5769 bp in length
36272 4123 contig of 5852 bp in length
42224 48172 contig of 5949 bp in length
48273 52700 contig of 4428 bp in length
52801 57587 contig of 4787 bp in length
57688 61624 contig of 3937 bp in length
61725 67756 contig of 6032 bp in length
67857 71834 contig of 3978 bp in length
71935 78800 contig of 4866 bp in length
78901 81069 contig of 4169 bp in length
81170 81932 contig of 763 bp in length
82033 86213 contig of 4181 bp in length
86314 89537 contig of 3224 bp in length
89638 92372 contig of 2735 bp in length
92473 94979 contig of 2507 bp in length
95080 96272 contig of 1193 bp in length
96373 98109 contig of 1737 bp in length
98210 101030 contig of 2821 bp in length
101131 103760 contig of 2630 bp in length
103861 106330 contig of 2470 bp in length
106431 109601 contig of 2171 bp in length

QY	607	TTGCAGCCTCATGGAAAGGCCTCATTTGAAGTCCAACTTTTCCCCACCTTAACACCAAGAAC	666
Db	15447	TCGCAGCCTCACCGBAAAGGCCTCATTTGAAGTCCAACTTTTCCCCACCTTAACACCAAGAAC	15506
QY	667	GGGTTGAACCTCCACACTGCACCGTTCCCTGAGAGTGCAGCTAAATCTCCTTCAATCT	726
Db	15507	GGGTTGAACCTCCACACTGCACCGTTCCCTGAGAGTGCAGCTAAATCTCCTTCAATCT	15566
QY	727	AACCCACCCCTACACTTTCCACACTCAGGAATACATPCTGAATATATACCCAAAACTAAG	786
Db	15567	AACCCACCCCTACACTTTCCACACTCAGGAATACATPCTGAATATATACCCAAAACTAAG	15626
QY	787	CCCATAAAGCAGCCGACCCCTAGTGGTTAAACCCCTATACCTTGTCTCCTATGGGTGAGT	846
Db	15627	CCCATAAAGCAGCCCAACCCCTAGTGGTTAAACCCCTATACCTTGTCTCCTATGGGTGAGT	15686
QY	847	CTGTTCTTGGCGCGCGCTCTCTCTGCTTCCTCCCTTAGAGCTGACTGTGCTCAGC-CT	905
Db	15687	CTGTTCTTGGCGCGCGCTCTCTCTGCTTCCTCCCTTAGGGCTGACTGTGCTCAGCACT	15746
QY	906	GCCAGCTCTCACATGTGCTGTCTCCACCCCTCTGACTCCCTCCCTCAAGCTGCAGTGGGACTG	965
Db	15747	GCCATCTCTCACATGTGCTGTCTCCACCCCTCTGACTCCCTCCCTCAAGCTGCAGTGGGACTG	15806
QY	966	GAAGACTGGCAGGAAGCTAGGTAACAACCTGGAACAACAGCAGGTCGACCTGCAGTCCCTTA	1025
Db	15807	GAAGACTGGCAGGAAGCTAGGTTACAACCTGGAACAACAGCAGGTCGACCTGCAGTCCCTTA	15866
QY	1026	GGCCTGGCCCGCTCCCTCCATGTACACATATACATGTTGGCACACACAGTGGGCACA	1085
Db	15867	GGCCTGGCCCGCTCCCTCCATGTACACATATACATGTTGGCACACACAGTGGGCACA	15926
QY	1086	CATGCCAAAAGACTCTCTCAGCTGACACACAGATCCATCTCAAGTATCTACTGTATAGACA	1145
Db	15927	CATGCCAAAAGACTCTCTCAGCTGACACACAGATCCATCTCAAGTATCTACTGTATAGACA	15986
QY	1146	CTCATGGTGCAGGTCTCATCTCTCAACATPACACATGCTCTTTCTCTCCCGTCTT	1205
Db	15987	CTCATGGTGCAGGTCTCATCTCTCAACATPACACATGCTCTTTCTCTCTCCCGTCTT	16046
QY	1206	GCCAGGAGTGTTCCTCTCTCATCCCTCTCGCTCCCATCTGTGTGCCACCCCTCACC	1265
Db	16047	GCCAGGAGTGTTCCTCTCTCATCCCTCTCGCTCCCATCTGTGTGCCACCCCTCACC	16106
QY	1266	CCCCACCCAGCCCAAGTGGGGACAGACACCTGAGGGGTGGCAGCTGCTTCCCGGTGTG	1325
Db	16107	CCCCACCCAGCCCAAGTGGGGACAGACACCTGAGGGGTGGCAGCTGCTTCCCGGTGTG	16166
QY	1326	GGCCCGGGCGCGCTCATGCTTCTGCTCCATCCCTGCCACAGGGGACTCGTGGGGGATGT	1385
Db	16167	GGCCCGGGCGCGCTCATGCTTCTGCTCCATCCCTGCCACAGGGGACTCGTGGGGGATGT	16226
QY	1386	TAGCGTGCCTGTGACAGGTGCTCTGGCACCTCCCTGCAGTGCAGCTCTCAATCGCACAG	1445
Db	16227	TAGCGTGCCTGTGACAGGTGCTCTGGCACCTCCCTGCAGTGCAGCTCTCAATCGCACAG	16286
QY	1446	GGGACCCAGGCCTGCCCTCTCATCTCCAGAAAACCTATGACCTCACCCGCTACCTGGAGC	1505
Db	16287	GGGACCCAGGCCTGCCCTCTCATCTCCAGAAAACCTATGACCTCACCCGCTACCTGGAGC	16346
QY	1506	ACCAACTCCGACCTTGGCTGGGACCTATGTCAAGTATCCAGGTAGGAATCTGGGAGTTG	1565
Db	16347	ACCAACTCCGACCTTGGCTGGGACCTATGTCAAGTATCCAGGTAGGAATCTGGGAGTTG	16406
QY	1566	GGGAGAGTGAGAGTTGGGAAAGACAGTCTTAACCGTGGAGGTTCTGGTAAATGATG	1625
Db	16407	GGGAGAGTGAGAGTTGGGAAAGACAGTCTTAACCGTGGAGGTTCTGGTAAATGATG	16466
QY	1626	GGGTGAGGAGGGGCTCTTTGGGCTCCACAGTCCCGCTGTGTGTTCTATCTCCTGCCCTT	1685
Db	16467	GGGTGAGGAGGGGCTCTTTGGGCTCCACAGTCCCGCTGTGTGTTCTATCTCCTGCCCTT	16526
QY	1686	CCCTCTTAGTGTGCCCCCCCACCTTCCCATCCCTGGCCCCAGGACTAGGCAATGTGGGCAG	1745

DB	16527	CCCTCTTAGTGTGGCCCCCCCACCTTCCCATCCCTGGCCCCAGGACTATGGCATATGGGGCAG	16586
QY	1746	GCCTTCGACACCGCCTTTGGGCCCATTTGCCCACTGGCTGCAGACCACGCGCCGCTCTCCC	1805
DB	16587	GCCTTCGACACCGCCTTTGGGCCCATTTGCCCACTGGCTGCAGACCACGCGCCGCTCTCCC	16646
QY	1806	CTGGGGCCCGGGAAAGTCTCTCTGTATTACCGTTGTTGGTGTCTCTTGGCGGGCGG	1865
DB	16647	CTGGGGCCCGGGAAAGTCTCTCTGTATTACCGTTGTTGGTGTCTCTTGGCGGGCGG	16706
QY	1866	GGTTGGGTGGGGACAGAGGGGCCACCTCCCATCCCTGCGTTCCAGCTCGCCTCTGCCC	1925
DB	16707	GGTTGGGTGGGGACAGAGGGGCCACCTCCCATCCCTGCGTTCCAGCTCGCCTCTGCCC	16766
QY	1926	CCAGACCTGGGGCCCTGTGCTCTGTGACCCAGGGCCCTCCCTTCGGTGTGCTCTCCCAT	1985
DB	16767	CCAGACCTGGGGCCCTGTGCTCTGTGACCCAGGGCCCTCCCTTCGGTGTGCTCTCCCAT	16826
QY	1986	CCTAGCTGGGCCCTTAGGGGGGTCTATGGGGGAAGGGGACTGTAGGGAACCCAGGCAGTA	2045
DB	16827	CCTAGCTGGGCCCTTAGGGGGGTCTATGGGGGAAGGGGACTGTAGGGAACCCAGGCAGTA	16886
QY	2046	GTGCGAGGGGGTTTAGGGTGTGAGATGGAGTTATGCTCTAAGATTTCGGGGTGGTCCAG	2105
DB	16887	GTGCGAGGGGGTTTAGGGTGTGAGATGGAGTTATGCTCTAAGATTTCGGGGTGGTCCAG	16946
QY	2106	AGTGTGTCAGAGAGCCAGGAGAGAAGNAGSAGGGTTGGAGGACCGAGGACCATGGG	2165
DB	16947	AGTGTGTCAGAGAGCCAGGAGAGAAGNAGSAGGGTTGGAGGACCGAGGACCATGGG	17005
QY	2166	GAACCGGGCCCTCTTCCCGTGTCTCTTCCACATCCAGACCTACTCTGGAGGCCAGG	2225
DB	17006	GAACCGGGCCCTCTTCCCGTGTCTCTTCCACATCCAGACCTACTCTGGAGGCCAGG	17065
QY	2226	GAAGAAGAGGAGAGAGTGTCGGGGGAGCTGGTCCAGCCCCAGGATACACGAGGAA	2285
DB	17066	GAAGAAGAGGAGAGGAGTGTCGGGGGAGCTGGTCCAGCCCCAGGATACACGAGGAA	17125
QY	2286	ATTAGTTGTGCTCTGTGCTTGTACAGCTGTGAACCTCCCTCGGGCCCTTGCCTATCCCA	2345
DB	17126	ATTAGTTGTGCTCTGTGCTTGTACAGCTGTGAACCTCCCTCGGGCCCTTGCCTATCCCA	17185
QY	2346	GGCCTCTCCGCTTGTCTTCCCTCTTTCGCCAGTTATACATCTCCCTCATCCCTTCCCT	2405
DB	17186	GGCCTCTCCGCTTGTCTTCCCTCTTTCGCCAGTTATACATCTCCCTCATCCCTTCCCT	17245
QY	2406	GGG-CCGACGCGCTCCCCGAGGGTTGGAAAGGCTCTGCCCTCTTCCCTATACCATGC	2464
DB	17246	GGGCCCCACGCGCTCCCCGAGGGTTGGAAAGGCTCTGCCCTCTTCCCTATACCATGC	17305
QY	2465	TGTCTCCATAGCCTTCCCTCTCTACTCATGAGCTGGCTCCATTTCTCTCTCTGC	2524
DB	17306	TGTCTCCATAGCCTTCCCTCTCTACTCATGAGCTGGCTCCATTTCTCTCTCTGC	17365
QY	2525	AACCTGCTCCTATCAGCTGAACCCCTCTTTGGAGTGTTAGTGAGTACCGHCTCTCCC	2584
DB	17366	AACCTGCTCCTATCAGCTGAACCCCTCTTTGGAGTGTTAGTGAGTACCGHCTCTCCC	17425
QY	2585	CAGCCCTCAGCTGTGGGCCCTGGGTGTGTCAGGGGCAATGGGGCTCTGTTTCCCATGG	2644
DB	17426	CAGCCCTCAGCTGTGGGCCCTGGGTGTGTCAGGGGCAATGGGGCTCTGTTTCCCATGG	17485
QY	2645	GCACCTCTCATCTCTCTTGTCTTGTGTGAGAAAACCTTTGTCTCACTCCATGCCCC	2704
DB	17486	GCACCTCTCATCTCTCTTGTCTTGTGTGAGAAAACCTTTGTCTCACTCCATGCCCC	17545
QY	2705	CTCTAGTTCGACCGCTTTTCTCTCTGGGCTTTCCCTGCCAATTTCTCGAGGAGTGG	2764
DB	17546	CTCTAGTTCGACCGCTTTTCTCTCTGGGCTTTCCCTGCCAATTTCTCGAGGAGTGG	17605
QY	2765	TCTACACCTCTGCTCCACTTCTCTCCACCCACTCACTTCTTAAACCCCTGCAATCTG	2824

17606	TCATCACCCCTCTGCTCTCCACTCTCTCTCCACCCCACTCACTTCTCTTAAACCCCTCGAATCTG	17666
2825	GCTTCCAGGCCCCAGCAATGGTTCTCTCCAAAGTTCGTGAGGCACCTCTTGTCCCAAGCCCG	2884
17666	GCTTCCAGGCCCCAGCAATGGTTCTCTCCAAAGTTCGTGAGGCACCTCTTGTCCCAAGCCCG	17725
2885	ACAGTGTTTTGAAGGCTCATCTCTCTTGGTCTGTCTTTTGGAGCCACACACTGCTCAGCGCT	2944
17726	ACAGTGTTTTGAAGGCTCATCTCTCTTGGTCTGTCTTTTGGAGCCACACACTGCTCAGCGCT	17785
2945	GCTGCTCTTCGAATCCCTCTTCCCTTGGTCTCTGCACTCTCTCTGGCCACACCTTCTACCTC	3004
17786	GCTGCTCTTCGAATCCCTCTTCCCTTGGTCTCTGCACTCTCTCTGGCCACACCTTCTACCTC	17845
3005	TCAGTCTCTCCAGGCTCTCTCTCTCTCTGTCCTGTCCTGCCCCACAGCGGGCACTCTCCAA	3064
17846	TCAGTCTCTCCAGGCTCTCTCTCTCTGTCCTGTCCTGCCCCACAGCGGGCACTCTCCAA	17905
3065	GGTTTGGCCACCCAGCAATCAGCAGCTCTCTCTCTGAGGCTCTTGTGGTCTCTCTCTCTCC	3124
17906	GGTTTGGCCACCCAGCAATCAGCAGCTCTCTCTCTGAGGCTCTTGTGGTCTCTCTCTCTCC	17964
3125	TCCTTTTCTACGCCCTCTCCATTGGAGAGCTCACACGCCCACTCTCTTCAACTGTCACCT	3184
17965	TCCTTTTCTACGCCCTCTCCATTGGAGAGCTCACACGCCCACTCTCTTCAACTGTCACCT	18024
3185	GCATCAAAATGATATCTTTATTTGAAAACACTCAGGAGGCCATGAACAAAGAGCCTAGC	3244
18025	GCATCAAAATGATATCTTTATTTGAAAACACTCAGGAGGCCATGAACAAAGAGCCTAGC	18084
3245	ATGGACACAGGGCCAGTGTCAAGGACACAAAAATAGAAAATTTTGGGAGCAGGTATCTC	3304
18085	ATGGACACAGGGCCAGTGTCAAGGACACAAAAATAGAAAATTTTGGGAGCAGGTATCTC	18144
3305	CTTGTGTGTGAGCCAGCGCTCTGCCCTCTCTCTTCCCAATCACCTCTCTTTTTCACAG	3364
18145	CTTGTGTGTGAGCCAGCGCTCTGCCCTCTCTCTTCCCAATCACCTCTCTTTTTCACAG	18204
3365	CTGAATCTACTGGGCCCCCTCTTCAACAGACAGACTTCAACCCCTCCCGCTCGGGGCA	3424
18205	CTGAATCTACTGGGCCCCCTCTTCAACAGACAGACTTCAACCCCTCCCGCTCGGGGCA	18264
3425	GAGACTCTGCCACAGGCCACTGTGTGACTTTGGAGGTGTGGCAAGCTCAATGACAAAATG	3484
18265	GAGACTCTGCCACAGGCCACTGTGTGACTTTGGAGGTGTGGCAAGCTCAATGACAAAATG	18324
3485	CGGCTGACCCAGAACTACAGAGCCTACAGGCACCTTCTGTGTACTTGGTGCGCCTCAAC	3544
18325	CGGCTGACCCAGAACTACAGAGCCTACAGGCACCTTCTGTGTACTTGGTGCGCCTCAAC	18384
3545	CGTCAGGCTGCCACTGCTGAGCTGCGCCGAGCGCTGGCCCACTCTGCAACCAAGCTCCAG	3604
18385	CGTCAGGCTGCCACTGCTGAGCTGCGCCGAGCGCTGGCCCACTCTGCAACCAAGCTCCAG	18444
3605	GGCCTGTGGGAGAGATATGGGGGCTATGGCAGCTCTGGGCTACCCACTGCCCAGCGG	3664
18445	GGCCTGTGGGAGAGATATGGGGGCTATGGGAGCTCTGGGCTACCCACTGCCCAGCGG	18504
3665	CTGCTGGGACTGAAACCCACTTGGACTCTCTGGCCCTGCCCAAGTACTTCTCCAGAAG	3724
18505	CTGCTGGGACTGAAACCCACTTGGACTCTCTGGCCCTGCCCAAGTACTTCTCCAGAAG	18564
3725	ATGGACGACTTCTGGTGTGTGAAGGAGCTGCAGACTGGCTGTGGGCTTGGGCCAAGNAC	3784
18565	ATGGACGACTTCTGGTGTGTGAAGGAGCTGCAGACTGGCTTGTGGGCTTGGGCCAAGNAC	18624
3785	TTCAAACCGGCTCAGAGAGAGATGACGCTTCCAGCAGCTGCAGTCACTCTGCACTTGGG	3844
18625	TTCAAACCGGCTCAGAGAGAGATGACGCTTCCAGCAGCTGCAGTCACTCTGCACTTGGG	18684
3845	GCTCATGGCTTCTGACTTCTGACCTTCTCTCTTCTGCTCTCCCTTCAAAACCTGTCTCCA	3904
18685	GCTCATGGCTTCTGACTTCTGACCTTCTCTCTTCTGCTCTCCCTTCAAAACCTGTCTCCA	18744

Qy	3905	CTTTGTGAGAGCAGCCCTGTATGCCAACCTGTTGAGCCAGAGACAGAGCTGTGAG	3964
Db	18745	CTTTGTGAGAGCAGCCCTGTATGCCAACCTGTTGAGCCAGAGACAGAGCTGTGAG	18804
Qy	3965	CTCTGGCCCTTTCTTGACCCGGCTGGGCGGTGTGATGCGATCAGCCCTGTCTCCTCCCA	4024
Db	18805	CTCTGGCCCTTTCTTGAGCCGGCTGGGCGGTGTGATGCGATCAGCCCTGTCTCCTCCCA	18864
Qy	4025	CTTCCAAAGGCTTACCGAGCTGGGAGGAGGTACAGTAGGCCCTGTCCGTGCTGTTTC	4084
Db	18865	CTTCCAAAGGCTTACCGAGCTGGGAGGAGGTACAGTAGGCCCTGTCTGCTGCTGTTTC	18924
Qy	4085	TACAGGAAGTCATGCTCGAGGGAGTGTGAAGTGGTTCAGGTTGGTGGCAGAGCGCTCATG	4144
Db	18925	TACAGGAAGTCATGCTCGAGGGAGTGTGAAGTGGTTCAGGTTGGTGGCAGAGCGCTCATG	18984
Qy	4145	GCCTCTGCTTCTTGCTTACCACTTGGCCAGTGGCCACCAGCCCTCAGGTGGCACAATC	4204
Db	18985	GCCTCTGCTTCTTGCTTACCACTTGGCCAGTGGCCACCAGCCCTCAGGTGGCACAATC	1904
Qy	4205	TGAGGGCAGGGGTTGAGGGGCCACCAACACATGCTTCTGGGGTGAAGCCCTTTGG	4264
Db	19045	TGAGGGCAGGGGTTGAGGGGCCACCAACACATGCTTCTGGGGTGAAGCCCTTTGG	19104
Qy	4265	CTGCCCCACTCTCTTGGATGGGTGTGCTCCCTTATCCCCAATCACTCTATACATCCA	4324
Db	19105	CTGCCCCACTCTCTTGGATGGGTGTGCTCCCTTATCCCCAATCACTCTATACATCCA	19164
Qy	4325	ATTTCAGGAACAAACATGTTGTGCAATTCTACACAAAAAGAGATTAGATTACAGTGCGG	4384
Db	19165	ATTTCAGGAACAAACATGTTGTGCAATTCTACACAAAAAGAGATTAGATTACAGTGCGG	19224
Qy	4385	GTTGGGGTCTGCATTGGAGGTGCCCTATAAACCAAGAGAGAAATACTGAAAGCACAAGGG	4444
Db	19225	GTTGGGGTCTGCATTGGAGGTGCCCTATAAACCAAGAGAGAAATACTGAAAGCACAAGGG	19284
Qy	4445	GCAGGACAGACACAGACCCAGGAGTCTCCAAAGCAGAGTGGCAAAACAAACCC	4504
Db	19285	GCAGGACAGACACAGACCCAGGAGTCTCCAAAGCAGAGTGGCAAAACAAACCC	19344
Qy	4505	GAGCTGAGCATCAGGACCTTGCTCGAATTGCTTCCAGTATTACGGTGCCCTCTCTCTG	4564
Db	19345	GAGCTGAGCATCAGGACCTTGCTCGAATTGCTTCCAGTATTACGGTGCCCTCTCTCTG	19404
Qy	4565	CCCCCTTTCCAGGGTATCTGTGGGTGCGAGGCTGGGAGGGCAACCATAGCCACCA	4624
Db	19405	CCCCCTTTCCAGGGTATCTGTGGGTGCGAGGCTGGGAGGGCAACCATAGCCACCA	19464
Qy	4625	CAGGATTTCTGAAAGTTTACAAATGACAGTAGCATTTTGGGGTGTAGGGTGCGAGCTCCCC	4684
Db	19465	CAGGATTTCTGAAAGTTTACAAATGACAGTAGCATTTTGGGGTGTAGGGTGCGAGCTCCCC	19524
Qy	4685	AAGGCCCTGCCCCAGCCCAACCATCAAGCTTAAGTGTGTGTATTAATTTAT	4744
Db	19525	AAGGCCCTGCCCCAGCCCAACCATCAAGCTTAAGTGTGTGTATTAATTTAT	19584
Qy	4745	TTATTTGGAGATGTTATTTATTTAGATGATTTATTTGACAGATTTCTATCTTGTATTAA	4804
Db	19585	TTATTTGGAGATGTTATTTATTTAGATGATTTATTTGACAGATTTCTATCTTGTATTAA	19644
Qy	4805	CAATAAAATGCTTGGCCCAAGAACTTAGTCTCTTTGGCCAGGCTCACCCCTCTCTGGTGCT	4864
Db	19645	CAATAAAATGCTTGGCCCAAGAACTTAGTCTCTTTGGCCAGGCTCACCCCTCTCTGGTGCT	19704
Qy	4865	CATCAGACTCTTGCCACCCCTGGCTCCCACTCCCTGCTTGCCTCTGTGGAGCTGCACAG	4924
Db	19705	CATCAGACTCTTGCCACCCCTGGCTCCCACTCCCTGCTTGCCTCTGTGGAGCTGCACAG	19764
Qy	4925	AGCTCTGGGAAGAGGCCCTTCTCTCCCGCAGCTGGGGCGATGGGGCGACCTCAGACTTA	4984
Db	19765	AGCTCTGGGAAGAGGCCCTTCTCTCCCGCAGCTGGGGCGATGGGGCGACCTCAGACTTA	19824

AUTHORS
TITLE
JOURNAL

Rat Genome Sequencing Consortium.
Direct Submission
Submitted (20-NOV-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

COMMENT

On Nov 20, 2002 this sequence version replaced gi:24270628.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.

----- Genome Center

Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: KCLS
Center clone name: CH230-42H20

----- Summary Statistics

Assembly program: Phrap; version 0.990329
Consensus quality: 212150 bases at least Q40
Consensus quality: 217133 bases at least Q30
Consensus quality: 220786 bases at least Q20
Estimated insert size: 230118; sum-of-contigs estimation
Quality coverage: 5x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 6 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 98082: contig of 98082 bp in length
* 98083 98182: gap of unknown length
* 98183 119083: contig of 20901 bp in length
* 119084 119183: gap of unknown length
* 119184 210852: contig of 91669 bp in length
* 210853 210953: gap of unknown length
* 210953 255663: contig of 44611 bp in length
* 255664 257428: gap of unknown length
* 257429 257528: gap of unknown length
* 257529 258710: contig of 1182 bp in length.

FEATURES

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KEYWORDS
JP 2002507125-A/1.
SOURCE
unidentified
ORGANISM
unclassified.
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1. (bases 1 to 1710)
AUTHORS
Shi X. and Ruben, S.M.
TITLE
Cardiotrophin-like cytokine
JOURNAL
Patent: JP 2002507125-A 1 05-MAR-2002;
HUMAN GENOME SCIENCES INC
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PN JP 2002507125-A/1
PD 05-MAR-2002
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 ACCESSION BC012939
 VERSION BC012939.1 GI:15277894
 KEYWORDS MGC.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 STRAUSBERG, R.L., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Klausner, R.D., Collins, F.S., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Altschul, S.F., Moore, T., Max, S.I., Wang, J., Hsieh, P., Hopkins, R.F., Jordan, H., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Datchenko, L., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scapleton, M., Brownstein, M.J., Ussid, T.B., Loquellano, N.A., Peters, G.J., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abranson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Warkley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalob, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahy, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Buffard, M.C., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalls, D.E., Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.
 Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 22388257
 12477932
 2 (bases 1 to 1736)
 Strausberg, R.
 Direct Submission
 Submitted (20-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
 NTH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgaps-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center
 Center code: BCM-HGSC
 Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
 Contact: amg@bcm.tmc.edu
 Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Lousseged, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAC Plate: 28 Row: b Column: 23
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 7019350.
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FEATURES
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Best Local Similarity 99.9%; Pred. No. 0;
Matches 1464; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3363 AGCTGAACACTCTGGGCCCCCTTCAACGAGCCAGACTTCAACCCCTCCCGCTGGGG 3422
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RESULT 13
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DEFINITION Homo sapiens cardiotrophin-like cytokine CLC mRNA, complete cds.
ACCESSION AF172854
VERSION AF172854.1 GI:5852980
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shi, X., Wang, W., Yourey, P.A., Gohari, S., Zukauskas, D., Zhang, J.,
Ruben, S. and Alderson, R.F.
Computational EST database analysis identifies a novel member of
TITLE

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the neurotrophic cytokine family
 JOURNAL Biochem Biophys. Res. Commun. 262 (1), 132-138 (1999)
 MEDLINE 99382254
 PUBMED 10448081
 REFERENCE 2 (bases 1 to 1689)
 AUTHORS Shi, Y.
 TITLE Direct Submission
 JOURNAL Submitted (28-JUL-1999) Molecular Biology, Human Genome Science,
 Inc., 9410 Key West Avenue, Rockville, MD 20850, USA
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ORIGIN

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 VERSION AX205024.1 GI:15394259
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 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Elson, G., Gauchat, J.F., Plum-Favreau, H., Chevalier, S. and Gascan, H.

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 15, 2004, 15:26:00 ; Search time 11579.5 Seconds
(without alignments)
13118.770 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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5: em_estov.*
6: em_estpl.*
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8: em_hcc.*
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29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c 2	860.2	16.9	1028	9	AL543945
c 3	755.4	14.8	773	14	CA430870
c 4	663.4	13.0	681	13	BU631799

c	5	656.6	12.9	681	10	AW978561	EST390670
c 6	637.4	12.5	679	14	CA306071	UI-H-Ft1-	
c 7	634.4	12.5	744	13	EX092291	EX092291	
c 8	618.2	12.2	675	14	CA748807	UI-H-Ft1-	
c 9	612	12.0	691	10	BF213570	601845370	
c 10	611.6	12.0	831	28	CC138171	NDL-3C1.T	
c 11	588	11.6	793	14	CK032835	AGENCOURT	
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c 13	577.8	11.4	763	14	CF271924	AGENCOURT	
c 14	576.8	11.3	801	14	CF271930	AGENCOURT	
c 15	572.8	11.3	800	14	CF271926	AGENCOURT	
c 16	567.4	11.2	915	10	BF035982	601457860	
c 17	540.2	10.6	806	14	CK130211	AGENCOURT	
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c 19	527	10.4	788	14	CF271927	AGENCOURT	
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c 26	490.6	9.6	662	29	AY409171	Pan trogl	
c 27	488.6	9.6	1157	13	BQ940483	AGENCOURT	
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c 38	437.2	8.6	465	9	AA430802	zw21a11.f	
c 39	429.4	8.4	432	9	AA430517	zw21a11.s	
c 40	422.4	8.3	432	9	AA278936	zw78d06.f	
c 41	422.2	8.3	433	9	AI765382	w174d07.x	
c 42	421.8	8.3	662	29	AY409172	Mus muscu	
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ALIGNMENTS

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DEFINITION
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clone CSODI004YMI5 3-PRIME, mRNA sequence.
ACCESSION
AL570325
VERSION
AL570325.2 GI:31291747
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EST.
SOURCE
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ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1025)
Li W.B., Gruber C., Jessee J., and Polayes D.
Full-length cDNA libraries and normalization
Unpublished (2001)
JOURNAL
On Feb 16, 2001 this sequence version replaced gi:12926520.
COMMENT
Contact: Genoscope
Genoscope - Centre National de Sequencage
Bp 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6127.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODI004AG08NP1&cluster=6127.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :

http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DI004AG08NP1.

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ORIGIN

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VERSION	AL5433945.2	GI:31265790			
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REFERENCE	1 (bases 1 to 1028)				
AUTHORS	Li, W.B., Gruber, C., Jessee, J. and Polayes, D.				
TITLE	Full-length cDNA libraries and normalization				
JOURNAL	Unpublished (2001)				
COMMENT	On Feb 15, 2001 this sequence version replaced qi:12875424.				

more information about this. <http://www.genoscope.cns.fr/>
<http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS001P004AG08Q1&cluster=6127.r>. Contact :
 Feng Liang Email : liang@lifetech.com URL :
<http://fulllength.invitrogen.com/> Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CS001P004AG08Q1.

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RESULT 4

BU631799/c
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 1 (bases 1 to 681)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaps-remail.nih.gov
 Tissue procurement: James Martin
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be obtained
 from Dr. M. Bento Soares, bento-soares@uiowa.edu
 Seq primer: M13 FORWARD
 POLYA=yes.

FEATURES

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 Site 2: Not I; NCI CGAP FLO is a cDNA library derived from
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 chondrosarcoma tissues. The library was constructed
 according to Bonaldo, Lennon and Soares, Genome Research,
 6:791-806, 1996. First strand cDNA synthesis was primed
 with an oligo-dT primer containing a Not I site. Double
 stranded cDNA was ligated to an EcoR I adaptor, digested
 with Not I, and cloned directionally into pT73-Pac
 vector. The oligonucleotide used to prime the synthesis of
 first-strand cDNA contains a library tag sequence that is

located between the Not I site and the (dT)18 tail. The
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 was provided by Dr. James Martin from University of Iowa.
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 TAG_SEQ=GAGTGGTG"

ORIGIN

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 QY 4223 GGGCCACACACACATGCTTCTGGGGTGAAGCCCTTGGCTGCCCACTCTCTCTGG 4282
 Db 621 GGGCCACACACATGCTTCTGGGGTGAAGCCCTTGGCTGCCCACTCTCTCTGG 562
 QY 4283 ATGGGTGTGCTCCCTTATCCCAATCACTCTATACATCCAAATCAGAAAAACAATG 4342
 Db 561 ATGGGTGTGCTCCCTTATCCCAATCACTCTATACATCCAAATCAGAAAAACAATG 502
 QY 4343 GTGGCAATCTACAAAAAGAGATGAGATTACAGTGCAGGGTGGGTCTGCATTGA 4402
 Db 501 GTGGCAATCTACAAAAAGAGATGAGATTACAGTGCAGGGTGGGTCTGCATTGA 442
 QY 4403 GGTGCCCTATAAACACAGAGAAAAATAGTGAAGACACAGGGGCGAGGACAGACACC 4462
 Db 441 GGTGCCCTATAAACACAGAGAAAAATAGTGAAGACACAGGGGCGAGGACAGACACC 382
 QY 4463 AGACCCAGGAGTCTCCAAAGCACAGATGGGCMAAAGCAAAACCCAGAGCTGAGATCAGGACC 4522
 Db 381 AGACCCAGGAGTCTCCAAAGCACAGATGGGCMAAAGCAAAACCCAGAGCTGAGATCAGGACC 322
 QY 4523 TTGCCTCGAATGCTCTCCAGTATTACGGTGCCTCTCTCTGCCCTCTTCCAGGGTAT 4582
 Db 321 TTGCCTCGAATGCTCTCCAGTATTACGGTGCCTCTCTCTGCCCTCTTCCAGGGTAT 262
 QY 4583 CTGTGGGTTGCCAGGCTGGGGAGGGCAACATAGCCACACACAGATTTCTGAAAGTT 4642
 Db 261 CTGTGGGTTGCCAGGCTGGGGAGGGCAACATAGCCACACACAGATTTCTGAAAGTT 202
 QY 4643 TACAATGCAGTACATTTTGGGGTGTAGGGTGGCAGCTCCCAAGGCCCTGCCCCAGC 4702
 Db 201 TACAATGCAGTACATTTTGGGGTGTAGGGTGGCAGCTCCCAAGGCCCTGCCCCAGC 142
 QY 4703 CCCACCCACTCATGACTCTAAGTGTGTTGATTAATTTATTATTGGAGATGTTAT 4762
 Db 141 CCCACCCACTCATGACTCTAAGTGTGTTGATTAATTTATTATTGGAGATGTTAT 82
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 QY 4823 CAGAA 4827
 Db 21 CAGAA 17

RESULT 5

AW978561/c
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 681)

AUTHORS Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holt, I. E., Saeed, A. I., Sharov, V., Lee, N. H., Yeatman, T. J. and Quackenbush, J.

TITLE Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray

JOURNAL Unpublished (2000)

COMMENT The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
Email: johnq@tigr.org
Plate: 394
Seq primer: Forward.

FEATURES

source	1. .681	Location/Qualifiers
	/organism="Homo sapiens"	
	/mol_type="mRNA"	
	/db_xref="taxon:9606"	
	/clone_lib="MAGE resequences, MAGP"	
	/note="Vector: pbluescriptSKm"	

ORIGIN

Query Match	12.9%;	Score 656.6;	DB 10;	Length 681;
Best Local Similarity	99.3%;	Pred. No. 1.3e-131;		
Matches	670;	Conservative 0;	Mismatches 4;	Indels 1; Gaps 1;

Qy 190 TGATACCTAAACCCGACCAAGTCACAGCCCTCCAACTCACCTCTGCTGCGCCAGACTCA 249

Db 681 TAATACCTAAACCCGACCAATTCACAGCTTCCAACTCACCTCTGCTGCGCCAGACTCA 622

Qy 250 CCACATCTTG-TGGACTCAAACTCAACGCGACTAAATCAACCAATCCCAAGTCTAA 308

Db 621 CCACATCTTG-TGGACTCAAACTCAACGCGACTAAATCAACCAATCCCAAGTCTAA 562

Qy 309 CTAATCTGAACCTTTTAAAGTAACCCAGTCTTAAACCTTAACCTAGCCCAATGCCAATTA 368

Db 561 CTAATCTGAACCTTTTAAAGTAACCCAGTCTTAAACCTTAACCTAGCCCAATGCCAATTA 502

Qy 369 TATACCTAGCAAAACCTTAAGTCTTGCGAGTCCAAAGTGTCCATGAATCTCTCA 428

Db 501 TATACCTAGCAAAACCTTAAGTCTTGCGAGTCCAAAGTGTCCATGAATCTCTCA 442

Qy 429 CCTTGGTCTCACTGAAATCCGAAAGCATATTTCCCACTGCCCCACATCCCTCTT 488

Db 441 CCTTGGTCTCACTGAAATCCGAAAGCATATTTCCCACTGCCCCACATCCCTCTT 382

Qy 489 ACAGCACCACCAACCTGCGCTCTGACCTCTGGATCTCTGGGATGTCCAAACTCTGCAGTG 548

Db 381 ACAGCACCACCAACCTGCGCTCTGACCTCTGGATCTCTGGGATGTCCAAACTCTGCAGTG 322

Qy 549 CCATCAGCAACAGCCGAGTGTCAATGACCTCTCTCCCTTCTGTCGCCACCTT 608

Db 321 CCATCAGCAACAGCCGAGTGTCAATGACCTCTCTCCCTTCTGTCGCCACCTT 262

Qy 609 GCAGGCTGATGGAAGGCTCATTGAAGTCAACTTTTCCCACTTAACCAAGAACGG 668

Db 261 GCAGGCTGATGGAAGGCTCATTGAAGTCAACTTTTCCCACTTAACCAAGAACGG 202

Qy 669 GGTGAACCTCCACTGCGACCTGCTGAGAGTGAGCACTAAATCTCTTCAATCTAA 728

Db 201 GGTGAACCTCCACTGCGACCTGCTGAGAGTGAGCACTAAATCTCTTCAATCTAA 142

Qy 729 CCCCACCTTCACTTTCCCACTCAGGAATCACATCTCTAGATATATACCAAACTAAGCC 788

Db 141 CCCCACCTTCACTTTCCCACTCAGGAATCACATCTCTAGATATATACCAAACTAAGCC 82

Qy 789 CCATAAGSCAGCCGACCTAGTGGTCTTAACCCCTATACCTTGTCTTCTATGGGTGAGTCT 848

Db 81 CCATAAGSCAGCCGACCTAGTGGTCTTAACCCCTATACCTTGTCTTCTATGGGTGAGTCT 22

Qy 849 GTTCTTGGCGGCGC 863

Db 21 GTTCTTGGCGGCGC 7

RESULT 6

CA306071 679 bp mRNA linear EST 01-NOV-2002

UI-H-Ftl-bhs-e-13-0-UI-s1 NCI CGAP Ftl Homo sapiens cDNA clone

UI-H-Ftl-bhs-e-13-0-UI 3', mRNA sequence.

CA306071

CA306071.1 GI:24469122

ESI.

Homo sapiens (human)

Homo sapiens

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Gary W. Hunninghake, U of I

cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa

DNA Sequencing By: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu

Seq primer: M13 FORWARD

POLYA=Yes.

FEATURES

source	1. .679	Location/Qualifiers
	/organism="Homo sapiens"	
	/mol_type="mRNA"	
	/db_xref="taxon:9606"	
	/clone="UI-H-Ftl-bhs-e-13-0-UI"	
	/tissue_type="Aveolar Macrophage"	
	/dev_stage="Adult"	
	/lab_host="DH10B (Life Technologies)"	
	/clone_lib="NCI CGAP Ftl"	
	/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP Ftl is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GCCCATGGCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.	
	TAG TISSUE=Human Lung Aveolar Macrophage	
	TAG_LIB=UI-H-Ftl	
	TAG_SEQ=GGCCATGCCG	

ORIGIN

Query Match	12.5%;	Score 637.4;	DB 14;	Length 679;
Best Local Similarity	99.2%;	Pred. No. 2e-127;		
Matches	660;	Conservative 0;	Mismatches 3;	Indels 2; Gaps 2;

Qy 4165 CACTTGGCGAGTGGCCACCCAGCCCTCAGGTG-CGACATCTGGAGGCGAGGTTGAGG 4223

Db 679 CACTTGGCGAGTGGCCACCCAGCCCTCAGGTGCGNACATCTGGAGGCGAGGTTGAGG 620

Qy 4224 GGCCA-CCACCACACATGCTTCTGGGTGAAGCCCTTGGCTGCCACCTCTCTCTGG 4282

Db 619 GGCCACCCACACATGCTTCTGGGTGAAGCCCTTGGCTGCCACCTCTCTCTGG 560

QY 4283 ATGGGTGTTGCTCCTTATCCCAAAATCACTCTATATCAATTCAGGAAACAAACATG 4342
 Db |||||
 QY 559 ATGGGTGTTGCTCCTTATCCCAAAATCACTCTATATCAATTCAGGAAACAAACATG 500
 Db |||||
 QY 4343 GTGGCAATTTCTACACAAAAGAGATGAGATTAACTAGTGCAGGTTGGGGTCTGCAATTGGA 4402
 Db |||||
 QY 499 GTGGCAATTTCTACACAAAAGAGATGAGATTAACTAGTGCAGGTTGGGGTCTGCAATTGGA 440
 Db |||||
 QY 4403 GTGGCCCTATAAACCCAGAGAGAAAATACTGAAAGCAGAGGGGCGGAGGACAGACAGACC 4462
 Db |||||
 QY 439 GTGGCCCTATAAACCCAGAGAGAAAATACTGAAAGCAGAGGGGCGGAGGACAGACAGACC 380
 Db |||||
 QY 4463 AGACCCAGAGTCTCCAAAGCAGAGTGGGCAACAAAACCCGAGCTGAGCATCAGGACC 4522
 Db |||||
 QY 379 AGACCCAGAGTCTCCAAAGCAGAGTGGGCAACAAAACCCGAGCTGAGCATCAGGACC 320
 Db |||||
 QY 4523 TTGCCTCGAATTGCTCTCCAGTATTACGGTGGCTCTCTCTGCCCCCTTTCCCGGGTAT 4582
 Db |||||
 QY 319 TTGCCTCGAATTGCTCTCCAGTATTACGGTGGCTCTCTCTGCCCCCTTTCCCGGGTAT 260
 Db |||||
 QY 4583 CTGTGGGTTGCCAGGTGGGGAGGCGCAACCATAGCCACACACAGATTTCCTGAAAGTT 4642
 Db |||||
 QY 259 CTGTGGGTTGCCAGGTGGGGAGGCGCAACCATAGCCACACACAGATTTCCTGAAAGTT 200
 Db |||||
 QY 4643 TACAATGCAATGAGCAATTTGGGGTGTAGGGTGGAGCTCCCAAGGCCCTGCCCCCAGC 4702
 Db |||||
 QY 199 TACAATGCAATGAGCAATTTGGGGTGTAGGGTGGAGCTCCCAAGGCCCTGCCCCCAGC 140
 Db |||||
 QY 4703 CCCACCACTCATGACTCTAAAGTGTGTATTAATTAATTAATTAATTAATTAATTAATTAAT 4762
 Db |||||
 QY 139 CCCACCACTCATGACTCTAAAGTGTGTATTAATTAATTAATTAATTAATTAATTAATTAAT 80
 Db |||||
 QY 4763 TATTAGATGATATTATTTCAGAAATTTCTATTTCTGTATTAAACAATAAATGCTTGCCC 4822
 Db |||||
 QY 79 TATTAGATGATATTATTTCAGAAATTTCTATTTCTGTATTAAACAATAAATGCTTGCCC 20
 Db |||||
 QY 4823 CAGAA 4827
 Db |||||
 QY 19 CAAAA 15
 Db |||||

RESULT 7
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 LOCUS
 DEFINITION BX092291 NCI CGAP GCBI Homo sapiens cDNA clone IMAGE998N021747 ;
 IMAGE:713281, mRNA sequence.
 ACCESSION BX092291
 VERSION BX092291.1 GI:27825213
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 744)
 Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M.,
 Radelof, J., Schneider, D. and Korn, S.
 Human Unigeneset - RZPD3
 Contact: Ina Rolfs
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
 Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
 RZPD; IMAGE998N021747.
 RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
 Human Unigeneset - RZPD3 (RZPDLIB No.972)
 http://www.rzpd.de/CloneCards/cgi-bin/showlib.pl.cgi/response?libNo=972 Contact: Ina Rolfs
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
 Heubnerweg 6, D-14059 Berlin, Germany
 Tel: +49 30 32639 101
 Fax: +49 30 32639 111
 www.rzpd.de
 This clone is available royalty-free from RZPD;
 contact RZPD (clone@rzpd.de) for further information. Seq primer:

ML3r, Primer sequence: TTTCACACAGGAAACAGCTATGAC.
 Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
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 /tissue_type="germinal center B cell"
 /lab_host="DH10B"
 /clone_lib="NCI CGAP GCBI"
 /notes="Vector: pT73D-Pac (Pharmacia) with a modified
 polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
 was prepared from human tonsillar cells enriched for
 germinal center B cells by flow sorting (CD20+, Igd-),
 provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
 (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
 primed with a Not I - oligo(dT) primer
 [5'-TGTTACCAATCTGAAGTGGAGCGCGCTCATTTTCTTTT-3',
 Double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified pT73 vector. Library
 went through one round of normalization, and was
 constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN
 Query Match 12.5%; Score 634.4; DB 13; Length 744;
 Best Local Similarity 98.1%; Pred. No. 9.3e-127;
 Matches 683; Conservative 0; Mismatches 8; Indels 5; Gaps 4;
 QY 133 CAGGTTGAAACCCAACTAGCCCTCTCTTATACATGACAGAGCGCCCATCTGA 192
 Db 49 CAAGCTGAAACCCAACTAGCCCTCTCTTATACATGACAGAGCGCCCATCTGA 108
 QY 193 TACTAAACGACCAAGTACAGCCCTTCAACCTCTGCTCTGCCAGACCTCACCA 252
 Db 109 TACTAAACGACCAAGTACAGCCCTTCAACCTCTGCTCTGCCAGACCTCACCA 168
 QY 253 CATCCTTG-TGGACTCAAACCTCAACCGCACTAAATCAACCAAAATCCCAAGTCTAACTA 311
 Db 169 CATCCTTGCTGACTCAAACCTCAACCGCACTAAATCAACCAAAATCCCAAGTCTAACTA 228
 QY 312 ATCTGAACCTTTAAAGTAAACCCAGTCTTAAACCTAACTAGCCCAATGCCAATATATAT 371
 Db 229 ATCTGAACCTTTAAAGTAAACCCAGTCTTAAACCTAACTAGCCCAATGCCAATATATAT 288
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 Db 289 CTACCTTAGCCAAACCCCTAACTGCTCTTCCAGTCCAAAGTGTCCACTGAATCTCCTCCT 348
 QY 432 TGTCTCTCACTGAAATCCAGAAAGCATATTTCCCACTGCCACATCCCTCCTTACA 491
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 QY 552 TCAGCCAAACGAGCCGACTCTGTCATTAATGACCTCTCTCTCTCTCTCTCTCTCTCTCTCT 611
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 QY 612 GGCTGATGGAAGAGGCTCATTTGAAGTCCAACTTTTCCCACTTAAACCAAGAACCGGGT 671
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 QY 672 GAACCTTCAACACTGCGACCGTTCCTCTGAGAGTGAGCATTAAATCTCTTCAATCTTAACCC 731
 Db 589 GAACCTTCAACACTGCGACCGTTCCTCTGAGAGTGAGCATTAAATCTCTTCAATCTTAACCC 648
 QY 732 CACCTTACACTTCCCACTCAGGAATCACTA-TCCTAGAAATATACCCAAATCTAAG-CCC 789
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QY 790 CATAGGACGCCG--ACCGTAGTGTCTAACCTTA 823
Db 709 CATAAGCAGCCCGACCCCTTAGNGGTCTAACCTTA 744

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LOCUS UI-H-F11-bid-i-12-0-UI.s1 NCI_CGAP_F11 Homo sapiens CDNA clone
DEFINITION UI-H-F11-bid-i-12-0-UI 3', mRNA sequence.
ACCESSION CA748807
VERSION CA748807.1 GI:25569227
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 675)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
JOURNAL Tumor Gene Index
COMMENT Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapsb-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-F11-bid-i-12-0-UI"
/tissue_type="Aveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP_F11"
/notes="Organ: lung; Vector: p7773-Pac (Pharmacia) with a
modified polylinker; Site: 1: Scorer I; Site 2: Not I;
NCI CGAP F11 is a normalized cDNA library constructed from
a pool of 81 RNA samples from Alveolar Macrophages
challenged with different treatments. The library was
normalized according to Bonaldo, Lennon and Soares, Genome
Research, 6:791-806, 1996. First strand cDNA synthesis was
primed with an oligo-dT primer containing a Not I site.
Double stranded cDNA was ligated to an EcoR I adaptor,
digested with Not I, and cloned directionally into
p7773-Pac vector. The oligonucleotide used to prime the
synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
GCCATGCGG. The tissue was provided by Dr. Gary W.
Hunninghake of the University of Iowa.
TAG_L1IB=UI-H-F11
TAG_SEQ=GGCCATGCCG"

ORIGIN
Query Match 12.2%; Score 618.2; DB 14; Length 675;
Best Local Similarity 98.9%; Pred. No. 3e-123;
Matches 654; Conservative 0; Mismatches 3; Indels 4; Gaps 3;

QY 4171 GCAGTGCACCCAGCCCTCAGGTGGCAGCATCTGGAGGCGAGGGGTGAGGGGCCACC 4230
Db 674 GCCATGTCACCCAGCCGCTCA-CTGGCAATCTGGAGGCGAGGGTGA--GGGCCACC 618
QY 4231 ACCACACATGCCCTTTCTGGGGTGAAGCCCTTTGGCTGCCCACTCTCCTTGGATGGGTGT 4290

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Db 617 ACCACACAT-CCTTTCTGGGGTGAAGCCCTTTGGCTGCCCACTCTCCTTGGATGGGTGT 559
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Db 558 TCGTCCCTTTATCCCAATCACTCTATACATCCATTCAGGAAACAAACATGGTGGCAAT 499
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QY 4411 ATAAACCCAGAGAGAAAATACCTGAAAGACACAGGGGCGAGGACAGACACAGACCCAG 4470
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QY 4531 AATTGTCTTCCAGTATTACGGTGCCTTCTCTGCCCCCTTTCCAGGGTATCTGTGGT 4590
Db 318 AATTGTCTTCCAGTATTACGGTGCCTTCTCTGCCCCCTTTCCAGGGTATCTGTGGT 259
QY 4591 TGCAGGCTGGGGAGGGAACCATAGCCACACAGAGATTTCTGAAAGTTTACAATGC 4650
Db 258 TGCAGGCTGGGGAGGGAACCATAGCCACACAGAGATTTCTGAAAGTTTACAATGC 199
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Db 198 AGTAGCATTTTGGGGGTAGGGTGGCAGCTCCCAAGGCCCTGCCCCAGACCCCA 139
QY 4711 CTCATGACTCTAAGTGTGTGTATTAAATTTATTATTGAGATGTTATTATTAGAT 4770
Db 138 CTCATGACTCTAAGTGTGTGTATTAAATTTATTATTGAGATGTTATTATTAGAT 79
QY 4771 GATATTTATGAGAAATTTCTATTCTTGTATTAAACAAATAAATGCTGCCCCAGAACTT 4830
Db 78 GATATTTATGAGAAATTTCTATTCTTGTATTAAACAAATAAATGCTGCCCCAGAACTT 19
QY 4831 A 4831
Db 18 A 18

RESULT 9
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LOCUS 601845370F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4070560 5',
DEFINITION mRNA sequence.
ACCESSION BF213570
VERSION BF213570.1 GI:11107156
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 691)
AUTHORS NIH-MGC http://mgs.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapsb-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM914 row: 1 column: 17
High quality sequence stop: 637.
Location/Qualifiers
1..691
/organism="Homo sapiens"

FEATURES
source

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/mol_type="mrna"
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 /notes="Organ: bone marrow; Vector: pDNR-LIB (Clontech);
 Site_1: SfiI (ggcccctcgcc); Site_2: SfiI
 (ggccattatgccc); Double-stranded cDNA was prepared from
 cell line RNA. 5' and 3' adaptors were used in cloning as
 follows: 5' adaptor sequence: 5'-CACGCCATTATGCC-3' and
 3' adaptor sequence:
 5'-ATTCTAGAGCCCGAGCGCGCCGACATG-dT(30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size
 1.65 kb (range 0.9-4.0 kb). 14/15 colonies contained
 inserts by PCR. This library was enriched for full-length
 clones and was constructed by Clontech Laboratories (Palo
 Alto, CA)."

ORIGIN

Query Match 12.0%; Score 612; DB 10; Length 691;
 Best Local Similarity 94.5%; Pred. No. 6.7e-122;
 Matches 656; Conservative 0; Mismatches 35; Indels 3; Gaps 2;

Qy 3727 GGACGACTTCTGCTCTCGAAGAGCTGAGACCTGGCTGTGGCTGGCCCAAGACTT 3786
 Db 1 GGACGACTTCTGCTCTCGAAGAGCTGAGACCTGGCTGTGGCTGGCCCAAGACTT 60

Qy 3787 CACCGGCTCAGAAAGATCCAGCTCCAGCAGCTGAGTCAACCTGACCTGGGGGC 3846
 Db 61 CACCGGCTCAGAAAGATCCAGCTCCAGCAGCTGAGTCAACCTGACCTGGGGGC 120

Qy 3847 TCATGCTTCTGACTTCTGACCTTCTCCTCTGCTGCTCCCTTCAAACTGCTCCCACT 3906
 Db 121 TCATGCTTCTGACTTCTGACCTTCTCCTCTGCTGCTCCCTTCAAACTGCTCCCACT 180

Qy 3907 TTGTGAGACGACCTCTGATGCCAACCTGTTGAGCCAGAGACAGAGCTGTGAGCC 3966
 Db 181 TTGTGAGACGACCTCTGATGCCAACCTGTTGAGCCAGAGACAGAGCTGTGAGCC 240

Qy 3967 TCTGGGCTTCTCTGACCGCTGGCGGTGTGATGGATCAGCTGCTCTCTCCCACT 4026
 Db 241 TCTGGGCTTCTCTGACCGCTGGCGGTGTGATGGATCAGCTGCTCTCTCCCACT 300

Qy 4027 TCCAAAGGTCTACCGAGCTGGGGAGAGGTACAGTAGCCCTGCTGCTGCTGTTCTA 4086
 Db 301 TCCAAAGGTCTACCGAGCTGGGGAGAGGTACAGTAGCCCTGCTGCTGCTGTTCTA 360

Qy 4087 CAGGAAGTCTGCTCGAGGAGGTGTGAAGTGTTCAGTGTGTGAGAGGGCTCATGCT 4146
 Db 361 CAGGAAGTCTGCTCGAGGAGGTGTGAAGTGTTCAGTGTGTGAGAGGGCTCATGCT 420

Qy 4147 CTCCTGCTTCTTCCCTACCACTTGGCCAGTGCCCAACCCCTCAGGTGCAATCTG 4206
 Db 421 CTCCTGCTTCTTCCCTACCACTTGGCCAGTGCCCAACCCCTCAGGTGCAATCTG 480

Qy 4207 GAGGCGAGGGTGTGAGGGCCACCCACACATGCTTCTGGGGTGAAGCCCTTGGCT 4266
 Db 481 GAGGCGAGGGTGTGAGGGCCACCCACCACTGCTTCTGGGGTGAAGCCCTTGG-- 537

Qy 4267 GCCCCACTCTCTTGGATGGGTGTGCTCCCTTATCCCAATCACTCTATACATCCAA 4326
 Db 538 TGCCCCACTCTCTTGGATGGGTGTGCTCCCTTATCCCAATCACTCTATACATCCAA 597

Qy 4327 TCAGGAACAAACATGGTGGCAATCTACAAAAGAGATGAGATTACAGTGCAGGGT 4386
 Db 598 TCAGGAACAAACATGGTGGCAATCTACAAAAGAGATGAGATTACAGTGCAGGGT 657

Qy 4387 TGGGGTCTGCAITGGAGGTGCCCTATAAACACAGA 4420
 Db 658 TGGGGTCTGATGGAGGGGCTATAACAGAGAGA 691

RESULT 10
 CCL18171
 LOCUS
 DEFINITION NDL.3C1.77 Notre Dame Liverpool Aedes aegypti genomic clone
 NDL.3C1, genomic survey sequence.
 ACCESSION CCL18171
 VERSION CCL18171.1 GI:30007226
 KEYWORDS GSS.
 SOURCE Aedes aegypti (yellow fever mosquito)
 ORGANISM Aedes aegypti
 BUKARYOTA; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Necoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes;
 Stegomyia.
 REFERENCE 1 (bases 1 to 831)
 AUTHORS Loftus B., Shetty J., Knudson, D. and Severson, D.
 TITLE BAC end sequencing of Aedes aegypti
 JOURNAL Unpublished (2003)
 COMMENT Contact: Brendan Loftus
 Department of Eukaryotic Genomics
 TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-838-3543
 Fax: 301-838-0208
 Email: enta@tigr.org
 Library was provided by David Severson
 Seq primer: T7
 Class: BAC ends.

FEATURES

Location/Qualifiers
 source 1..831
 /organism="Aedes aegypti"
 /mol_type="genomic DNA"
 /strain="liverpool"
 /db_xref="taxon:7159"
 /clone="NDL.3C1"
 /clone_lib="Notre Dame Liverpool"
 /notes="Vector: pECBAC1; Site_1: Hind III; The library was
 prepared from whole body tissue of newly hatched L1 larvae
 by David Severson at the University of Notre Dame and
 Hongbin Zhang"

ORIGIN

Query Match 12.0%; Score 611.6; DB 28; Length 831;
 Best Local Similarity 85.9%; Pred. No. 8.9e-122;
 Matches 718; Conservative 0; Mismatches 104; Indels 14; Gaps 3;

Qy 3313 TGAGCCAGCGGCTCTGCCCTCTCTCCCTCCCACTCAACCTCCCGCTGGGGCAGACATC 3372
 Db 1 TTAGCTGGCTGTCTGGCCCTCTCCCTCCCACTCGCCCTCTCTTTTTCACAGCTTAAC 60

Qy 3373 CCTG-GGCCCCCTTTCAAGAGCCAGACTTCAACCTCCCGCTGGGGCAGACATC 3431
 Db 61 CCTGAGGCCCTTTTCAAGAACCTTCAACCTTCAACCTTGGCTGGGGCAGACATC 120

Qy 3432 TGCCCAAGGCGCACTGTGTGCTTGGAGGTGTGGCAAGCTCAATGACAACTCGGCTGA 3491
 Db 121 TGCCCAAGGCGCACTGTGTGCTTGGAGGTGTGGCAAGCTCAATGACAACTCGGCTGA 180

Qy 3492 CCAGAACTACGAGGCTTACAGCCACTTCTGTGTACTTGGTGGCTCAACCTGAG 3551
 Db 181 CCAGAACTACGAGGCTTACAGCCACTTCTGTGTACTTGGTGGCTCAACCTGAG 240

Qy 3552 CTGCCACTGTGAGCTGGCGCAGCTGCGCCACTTCTGCAACCTCCAGGGCTGCTG 3611
 Db 241 CCGCCACAGCCAGCTGGCGCAGCTGCGCCACTTCTGCAACCTCCAGGGCTGCTG 300

Qy 3612 TGGGACAGATTCGGGGCTCATGCGAGCTTGGGCTACCCACTGCCCCAGCGCTGCTG 3671
 Db 301 TGGGACAGATTCGGGGCTCATGCGAGCTTGGGCTACCCACTGCCCCAGCGCTGCTG 360

Qy 3672 GGACTGAACCACTTGGACTTCTTGGCCCTGCCACAGTGAATCTCTCCAGAAAGATGAG 3731
 Db 361 GGACTGAACCACTTGGACTTCTTGGCCCTGCCACAGTGAATCTCTCTCCAGAAAGATGAG 420

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 JOURNAL Tumor Gene Index
 COMMENT Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaps@mail.nih.gov
 Tissue Procurement: Dr. Gary W. Hunninghake, U of I
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be obtained
 from Dr. M. Bento Soares, bento-soares@uiowa.edu
 Seq primer: M13 FORWARD
 POLYA=yes.

FEATURES
 source
 1..606
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UI-H-F11-bid-a-09-0-UI"
 /tissue_type="Aveolar Macrophage"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies)"
 /clone_lib="NCI CGAP F11"
 /note="Organ: Lung; Vector: pVT3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI-CGAP F11 is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pVT3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (GT)18 tail. The sequence tag for this library is GCCATGCGG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.
 TAG_LIB=UI-H-F11
 TAG_SEQ=GGCCATGCGG"

ORIGIN
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 Best Local Similarity 99.8%; Pred No. 1.6e-114;
 Matches 589; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

4242 CTTTCTGGGGTGAAGCCCTTTGGCTGCCCACTCTCTTGGATGGGTGTGTCCTCTTAT 4301
 Db CTTTCTGGGGTGAAGCCCTTTGGCTGCCCACTCTCTTGGATGGGTGTGTCCTCTTAT 548
 4302 CCCCACATCACTATACATCAATTCAGGAACAAACATGTGGCAATTTACACAAA 4361
 Db CCCCACATCACTATACATCAATTCAGGAACAAACATGTGGCAATTTACACAAA 488
 4362 AGAGATGAGATTAACAGTGCAGGGTTGGGGTCTGCATTGGAGGTGCCCTATAAACAGAA 4421
 Db AGAGATGAGATTAACAGTGCAGGGTTGGGGTCTGCATTGGAGGTGCCCTATAAACAGAA 428
 4422 GAGAAATCTGAAGCAGGGGAGGACAGACAGACAGACAGACAGACAGACAGACAGACAG 4481
 Db GAGAAATCTGAAGCAGGGGAGGACAGACAGACAGACAGACAGACAGACAGACAGACAG 368
 4482 GCACAGATGGCAAAACAAACCCGAGCTGAGCATCAGGACCTTGCTCGAATTTGCTTCC 4541
 Db GCACAGATGGCAAAACAAACCCGAGCTGAGCATCAGGACCTTGCTCGAATTTGCTTCC 308
 4542 AGTATTACGGTGCCTTCTCTGCCCCCTTTCCAGGGTATCTGTGGTTCAGGCTGG 4601
 Db AGTATTACGGTGCCTTCTCTGCCCCCTTTCCAGGGTATCTGTGGTTCAGGCTGG 248

Qy 4502 GGAGGGCAACATAGGACACACACAGGATTTCTGAAGTTTCAATGAGTAGGATTTT 4561
 Db 247 GGAGGGCAACATAGGACACACACAGGATTTCTGAAGTTTCAATGAGTAGGATTTT 188
 Qy 4562 GGGGTGAGGGTGGCAGCTCCCAAGGCCCTGCCAGCCGCCAGCCGCCAGCTCATGACTCT 4721
 Db 187 GGGGTGAGGGTGGCAGCTCCCAAGGCCCTGCCAGCCGCCAGCCGCCAGCTCATGACTCT 128
 Qy 4722 AAGTGTGTTCTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 4781
 Db 127 AAGTGTGTTCTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 68
 Qy 4782 CAGAAATTTCTTCTTGTATTACAAATAAATGCTTGCCTGCCAGACTTA 4831
 Db 67 CAGAAATTTCTTCTTGTATTACAAATAAATGCTTGCCTGCCAGACTTA 18

RESULT 13
 CF271924/c
 LOCUS CF271924
 DEFINITION AGENCOURT_15197020 NIH_MGC_195 Homo sapiens cDNA clone
 IMAGE:7002181 5', mRNA sequence.
 ACCESSION CF271924
 VERSION CF271924
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 763)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT On Aug 12, 2003 this sequence version replaced gi:33627836.
 Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgaps@mail.nih.gov
 Tissue Procurement: Narayan Bhat
 cDNA Library Preparation: Bhat Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: IRBK4 row: e column: 11
 High quality sequence start: 7
 High quality sequence stop: 648.
 Location/Qualifiers
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:7002181"
 /tissue_type="mixed"
 /lab_host="DH5A (TI phage-resistant)"
 /clone_lib="NIH MGC 195"
 /notes="Vector: pDNR-Dual; Site 1: loxP-Sall; Site 2: loxP-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxP sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at

FEATURES
source

Db 196 ACTTCAACCGGCTCAGAGAGAGATGCAGCTCCAGAGAGTGCAGTCAACCTGCACTGG 137
 QY 3843 GGGCTCATGGCTTCTGACTTCTGACTTCTCTTGGTCCCTTCAAAACCTGCTCC 3902
 Db 136 GGGCTCATGGCTTCTGACTTCTGACTTCTCTTGGTCCCTTCAAAACCTGCTCC 77
 QY 3903 CACTTTGTGAGAGCAGCGCTGTATGCCAAACCTGTTGAGCAGGAGACAGAGCTGTG 3962
 Db 76 CAC-TTGTGAGAGCCAGGCC-GTATGCCAACCTGTTGAGCAGGAGACAGAGCTGTG 19
 QY 3963 AGCCT 3967
 Db 18 AGCCT 14

RESULT 15
 CF271926/c
 LOCUS
 DEFINITION AGENCOURT_15196988 NIH_MGC.195 Homo sapiens cDNA clone
 IMAGE:7002180 5', mRNA sequence.
 ACCESSION CF271926
 VERSION CF271926.2 GI:38453379
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 800)
 NIH-MGC <http://mgs.nci.nih.gov/>
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 On Aug 12, 2003 this sequence version replaced gi:33627838.
 Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgabs-r@mail.nih.gov
 Tissue Procurement: Narayan Bhat
 cDNA Library Preparation: Bhat Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: IRBK4 row: e column: 10
 High quality sequence start: 8
 High quality sequence stop: 720.
 Location/Qualifiers

FEATURES
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 1..800
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:7002180"
 /tissue_type="mixed"
 /lab_host="DH5A (T1 phage-resistant)"
 /clone_lib="NIH MGC 195"
 /note="Vector: pDNR-Dual; Site 1: loxp-SalI; Site 2:
 loxp-HindIII; clones from this library have been
 PCR-amplified using gene-specific primers to contain the
 complete open reading frame (based on known gene sequences
 available from NCBI's Refseq). Template for PCR is cDNA
 derived from either pooled cytoplasmic polyA RNA from 30
 cells lines or pooled total RNA from 10 different tissues
 (from BD Biosciences/Clontech and Washington University).
 PCR products are directionally cloned into the loxp sites
 of the pDNR-Dual vector. Library constructed by Dr.
 Narayan Bhat, Earl Bere III and Hongling Liao (Gene
 Expression Laboratory, Research Technology Program, SAIC
 Frederick, NCI-Frederick, Frederick, MD 21702). For
 information on which gene each clone represents, please
 visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearrayed_plates/IRBK_preSV.dat

ORIGIN
 Query Match 11.3%; Score 572.8; DB 14; Length 800;
 Best Local Similarity 99.3%; Pred. No. 2.4e-113;
 Matches 596; Conservative 0; Mismatches 2; Indels 2; Gaps 2;
 QY 3363 AGCTGAACCTACCTGGGCCCCCTTTTCAAGAGAGCAGACATTTCAACCTCCCGCTGGGG 3422
 Db 614 ATCTGAACCTACCTGGGCCCCCTTTTCAAGAGAGCAGACATTTCAACCTCCCGCTGGGG 555
 QY 3423 CAGAGACTCTGCCCCAGGGGCCACTGTTGACTTGGAGGTGTGGGAGCCCTCAATGACAAAC 3482
 Db 554 CAGAGACTCTGCCCCAGGGGCCACTGTTGACTTGGAGGTGTGGGAGCCCTCAATGACAAAC 495
 QY 3483 TGGGGCTGACCCAGAACTACGAGGCCCTACAGCCACCTTCTGTGTTTACTTGGCTGGCTCA 3542
 Db 494 TGGGGCTGACCCAGAACTACGAGGCCCTACAGCCACCTTCTGTGTTTACTTGGCTGGCTCA 435
 QY 3543 ACCGTGAGGTGCTGCACTGTGAGCTGGCGGAGCCCTGCGCCACCTTCTGCAACAGCTCC 3602
 Db 434 ACCGTGAGGTGCTGCACTGTGAGCTGGCGGAGCCCTGCGCCACCTTCTGCAACAGCTCC 375
 QY 3603 AGGGCTGTGGGCGAGCATTGGGGCGTCTATGSCAGCTCTGGGCTACCCACCTGCCCCAGC 3662
 Db 374 AGGGCTGTGGGCGAGCATTGGGGCGTCTATGSCAGCTCTGGGCTACCCACCTGCCCCAGC 315
 QY 3663 CGCTGCTGGGACTGAACCCACTTGGACTCTTGGCCCTGCCACAGTGAAGTCTTCTCCAGA 3722
 Db 314 CGCTGCTGGGACTGAACCCACTTGGACTCTTGGCCCTGCCACAGTGAAGTCTTCTCCAGA 255
 QY 3723 AGATGAGAGCTTCTGCTGCTGAAGAGCTGAGACCTGGCTGTGGCTGGCCAGG 3782
 Db 254 AGATGAGAGCTTCTGCTGCTGAAGAGCTGAGACCTGGCTGTGGCTGGCCAGG 195
 QY 3783 ACTTCAACCGGCTCAAGAGAGAGATGAGCCTCCAGCAGCTGAGTCAACCTGCACTGG 3842
 Db 194 ACTTCAACCGGCTCAAGAGAGAGATGAGCCTCCAGCAGCTGAGTCAACCTGCACTGG 135
 QY 3843 GGGCTCATGGCTTCTGACTTCTGACTTCTCTTGGCTCCCTTCAAAACCTGCTCC 3902
 Db 134 GGGCTCATGGCTTCTGACTTCTGACTTCTCTTGGCTCCCTTCAAAACCTGCTCC 75
 QY 3903 CACTTTGTGAGAGCAGCGCTGTATGCCAAACCTGTTGAGCAGGAGACAGAGCTGTG 3962
 Db 74 CACTTTGTGAGAGCAGCGCTGTATGCCAAACCTGTTGAGCAGGAGACAGAGCTGTG 17

Search completed: August 16, 2004, 04:01:38
 Job time : 11585.8 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 15, 2004, 12:15:49 ; Search time 1741.71 Seconds
(without alignments)
12407.700 Million cell updates/sec

Title: US-09-931-704-3

Perfect score: 5087

Sequence: 1 aacctggagtgccctggc.....cctttgctaagtcttctctca 5087

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_29Jan04.*

- 1: geneseq1980s.*
- 2: geneseq1990s.*
- 3: geneseq2000s.*
- 4: geneseq2001as.*
- 5: geneseq2001bs.*
- 6: geneseq2002s.*
- 7: geneseq2003as.*
- 8: geneseq2003bs.*
- 9: geneseq2003cs.*
- 10: geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5087	100.0	5087	3 AAA39482	AAA39482 Human NNT
2	5087	100.0	5087	6 ABK11648	ABK11648 Human nov
3	5076	99.8	5088	2 AAV22653	AAV22653 Human gen
4	5076	99.8	5088	2 AAV47511	AAV47511 Human neu
5	1484.4	28.8	1790	3 AAA88546	AAA88546 Human int
6	1463.4	28.8	1710	2 AAX16161	AAX16161 Human car
7	535.4	10.5	1008	4 AAK51548	AAK51548 Human pol
8	529.4	10.4	729	4 AAD04201	AAD04201 Human car
9	525.4	10.3	881	4 AAH74484	AAH74484 Nucleotid
10	523.4	10.3	797	2 AAV22652	AAV22652 cDNA enco
11	523.4	10.3	797	2 AAV47510	AAV47510 Human neu
12	523.4	10.3	797	3 AAA39481	AAA39481 Human NNT
13	523.4	10.3	797	6 ABK11647	ABK11647 Human cdn
14	495.4	9.7	968	4 ABA09140	ABA09140 Human car
15	495.4	9.7	968	4 AAK52532	AAK52532 Human pol
16	493.4	9.7	495	4 AAI25564	AAI25564 Probe #15
17	493.4	9.7	495	4 ABA71773	ABA71773 Human foe
18	493.4	9.7	495	4 AAI52108	AAI52108 Probe #20
19	493.4	9.7	495	4 ABA37855	ABA37855 Probe #16
20	493.4	9.7	495	4 AAK46202	AAK46202 Human bon
21	493.4	9.7	495	4 AAK20142	AAK20142 Human bra
22	493.4	9.7	495	4 ABA54921	ABA54921 Human liv
23	493.4	9.7	495	6 ABA20513	ABA20513 Human gen

24	492.4	9.7	768	4 AAH99772	AAH99772 Human pro
C 25	492	9.7	492	4 AAI16384	AAI16384 Probe #63
C 26	492	9.7	492	4 ABA59256	ABA59256 Human foe
C 27	492	9.7	492	4 AAI39047	AAI39047 Probe #77
C 28	492	9.7	492	4 ABA27986	ABA27986 Probe #64
C 29	492	9.7	492	4 AAK33253	AAK33253 Human bon
C 30	492	9.7	492	4 AAK07469	AAK07469 Human bra
C 31	492	9.7	492	4 ABA33003	ABA33003 Human liv
C 32	492	9.7	492	6 ABA08085	ABA08085 Human gen
C 33	437.2	8.6	465	6 ABL81689	ABL81689 Human ova
C 34	429.6	8.4	819	2 AAV22654	AAV22654 cDNA enco
C 35	429.6	8.4	819	2 AAV47512	AAV47512 Mouse neu
C 36	429.6	8.4	819	3 AAA39483	AAA39483 Murine NN
C 37	429.6	8.4	819	6 ABK11649	ABK11649 Mouse cdn
C 38	429.4	8.4	432	6 ABL81658	ABL81658 Human ova
C 39	421.8	8.3	648	3 AAA88547	AAA88547 Mouse int
C 40	398	7.8	457	8 ACH22723	ACH22723 Human adu
C 41	355.8	7.0	360	6 ABL79632	ABL79632 Human ova
C 42	330	6.5	342	2 AAX51546	AAX51546 Human sec
C 43	329	6.5	340	3 AAC14792	AAC14792 Human car
C 44	324.6	6.4	396	2 AAX16162	AAX16162 Human car
C 45	250.6	4.9	269	6 ABL82404	ABL82404 Human ova

ALIGNMENTS

RESULT 1
AAA39482
ID AAA39482 standard; DNA; 5087 BP.

AC AAA39482;

DT 24-AUG-2000 (first entry)

DE Human NNT-1 DNA.

XX NNT-1; human; neurotrophic factor; neurotrophic; neuroprotective; treatment;
XX anticonvulsant; antiparkinsonian; antidiabetic; ophthalmological;
XX nervous system degeneration; Alzheimer's disease; Parkinson's disease;
XX neurotrophic lateral sclerosis; Charcot-Marie-Tooth syndrome;
XX Huntington's disease; peripheral neuropathy; neural retina degeneration;
XX retinopathy; immune disorder; hematopoietic disorder; ss.

OS Homo sapiens.

PN US6054294-A.

PD 25-APR-2000.

XX 12-DEC-1997; 97US-00988819.

XX 03-FEB-1997; 97US-00792019.

PA (AMGE-) AMGEN INC.

PI Chang M;

XX WPI; 2000-338492/29.

PT New nucleic acids encoding neurotrophic factors useful for stimulating
growth of motor or sympathetic neurons for treating neuron cell damage.

XX Claim 1b; Col 31-36; 42pp; English.

CC This invention describes a novel nucleic acid molecule (I) encoding a
novel neurotrophic factor (NNT-1) (II) which has neurotrophic, antidiabetic and
neuroprotective, anticonvulsant, antiparkinsonian, antidiabetic and
ophthalmological activity. (I) is useful for producing NNT-1 polypeptides
which are useful for treating patients in whom various cells of the
central, autonomic, or peripheral nervous system have degenerated and/or
have been damaged by congenital disease, trauma, mechanical damage,
surgery, stroke, ischemia, infection, metabolic disease, nutritional

CC	deficiency, malignancy and/or toxic agents. NNT-1 proteins are used to
CC	treat diseases like Alzheimer's, Parkinson's, amyotrophic lateral
CC	sclerosis, Charcot-Marie-Tooth syndrome, Huntington's disease, peripheral
CC	neuropathy induced by diabetes or other metabolic disorders, and/or
CC	dystrophies or degeneration of the neural retina such as retinitis
CC	pigmentosa, drug-induced retinopathies, stationary forms of night
CC	blindness, progressive cone-rod degeneration, immune disorders and
CC	hematopoietic disorders. (I) is effective in treating neurological
CC	conditions and promotes neuron regeneration. Neural functions are
CC	effectively restored in patients suffering from various neurological
CC	disorders. This sequence encodes the human NNT-1 protein described in the
CC	method of the invention
XX	
SQ	Sequence 5087 BP; 992 A; 1746 C; 1191 G; 1158 T; 0 U; 0 Other;
Query Match	100.0%; Score 5087; DB 3; Length 5087;
Best Local Similarity	100.0%; Pred. No. 0;
Matches 5087; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 AACCTCGAGTGGGCTGGCGGATGGGATTATTAAAGCTTTGCGCGAGCGCGGCTCGCC 600
Db	1 AACCTCGAGTGGGCTGGCGGATGGGATTATTAAAGCTTTGCGCGAGCGCGGCTCGCC 60
Qy	61 CTCCTCACTCGGCAGGCTCCGGGAGAGCGGACCGCGCGCGCCAGCGCCAGCCGCCCCA 120
Db	61 CTCCTCACTCGGCAGGCTCCGGGAGAGCGGACCGCGCGCGCCAGCGCCGCCCCA 120
Qy	121 TGAACCTCGGAGAGGTTGAAACCCAAACTAGAGCCCTGCTTTCATTAACATGACAGCAG 180
Db	121 TGAACCTCGGAGAGGTTGAAACCCAAACTAGAGCCCTGCTTTCATTAACATGACAGCAG 180
Qy	181 CGGCCCATCTGATACTTAACCGCAACCAAGTCACAGCCCTCCAACTCACCTCTGCTCTGCC 240
Db	181 CGGCCCATCTGATACTTAACCGCAACCAAGTCACAGCCCTCCAACTCACCTCTGCTCTGCC 240
Qy	241 CAGACCTCCACCATCTTGTGGAGCTCAAACTCAACGGCACTAAATCAACCAAAATCCCA 300
Db	241 CAGACCTCCACCATCTTGTGGAGCTCAAACTCAACGGCACTAAATCAACCAAAATCCCA 300
Qy	301 AGTCTAAACTAATCTGAACCTTTTAAAGTAAACCGAGTCTTTAAACCTAACTAGCCCAAT 360
Db	301 AGTCTAAACTAATCTGAACCTTTTAAAGTAAACCGAGTCTTTAAACCTAACTAGCCCAAT 360
Qy	361 GCCAAATTATCTACCTTAGCCAAACCCCTAACTGCTCTTTGCGAGTCCAAAAGTGTCCACTG 420
Db	361 GCCAAATTATCTACCTTAGCCAAACCCCTAACTGCTCTTTGCGAGTCCAAAAGTGTCCACTG 420
Qy	421 AATCTCAACCTTGCTGCTCACTGAAAAATCCCGAAAAAGCATATTTCCGCACCTGCCACAT 480
Db	421 AATCTCAACCTTGCTGCTCACTGAAAAATCCCGAAAAAGCATATTTCCGCACCTGCCACAT 480
Qy	481 CCCTCTCTACAGCACCAACCTCGGCTCTGGAATCTGGATCTCTGGGATGTCCAAACT 540
Db	481 CCCTCTCTACAGCACCAACCTCGGCTCTGGAATCTGGATCTCTGGGATGTCCAAACT 540
Qy	541 CTCAGTGGCCATCAGCCAAACAGCCCGCATCGTCAAAATGCAACCTCTCTCCCTTCCTGTCC 600
Db	541 CTCAGTGGCCATCAGCCAAACAGCCCGCATCGTCAAAATGCAACCTCTCTCCCTTCCTGTCC 600
Qy	601 CCACCTTCGAGCTCATGGAAGGCGCTCATTTGAAGTCCAACTTTTCCCACTTAACACC 660
Db	601 CCACCTTCGAGCTCATGGAAGGCGCTCATTTGAAGTCCAACTTTTCCCACTTAACACC 660
Qy	661 AAGAAAGGGGTGAACCTCCACACTGCAACCGTTCCTCAGAGTGAGCACTAAATCTCCTT 720
Db	661 AAGAAAGGGGTGAACCTCCACACTGCAACCGTTCCTCAGAGTGAGCACTAAATCTCCTT 720
Qy	721 CAATCTTAACCCCACTTACACTTCCCACTCAGGAATCACTCTTAGAATATACCCAAA 780
Db	721 CAATCTTAACCCCACTTACACTTCCCACTCAGGAATCACTCTTAGAATATACCCAAA 780
Qy	781 ACTAAGCCCAATGAAGCAGCCGCAACCTAGTGGTCTAAACCCCTATACCTTGTCTTCTATGG 840

QY 1921 TGCCCCCAGACCTGGGGCCCTGCTCTGTGAGCCAGGGGCTCCCTTCGCTGCGCTCT 1980
DB 1921 TGCCCCCAGACCTGGGGCCCTGCTCTGTGAGCCAGGGGCTCCCTTCGCTGCGCTCT 1980
QY 1981 CCCATCTAGCTGGCCCTCCTAGGGGGTCTAGGGGGTGTGAGGGAGAGGAGCTGTAGGGAGAGCCAGG 2040
DB 1981 CCCATCTAGCTGGCCCTCCTAGGGGGTCTAGGGGGTGTGAGGGAGAGGAGCTGTAGGGAGAGCCAGG 2040
QY 2041 CAGTAGTGGCAGGGGGTGTAGGGTGTGATGGAGGTATGTGTAAAGATTTGGGGGTGG 2100
DB 2041 CAGTAGTGGCAGGGGGTGTAGGGTGTGATGGAGGTATGTGTAAAGATTTGGGGGTGG 2100
QY 2101 TCCAGAGTGTTCAGAGAGCCAGAGAGAGAGAGAGGGTGTGAGGAGCCGAGGACCC 2160
DB 2101 TCCAGAGTGTTCAGAGAGCCAGAGAGAGAGAGAGGGTGTGAGGAGCCGAGGACCC 2160
QY 2161 ATGGGGAACCGCCCCCTCTCCCGTGTCTCTTCCATCTCCAGAGCCCTACTCTGGAG 2220
DB 2161 ATGGGGAACCGCCCCCTCTCCCGTGTCTCTTCCATCTCCAGAGCCCTACTCTGGAG 2220
QY 2221 CCAGGGAAAGAAAGGGAGAGGTGGCGGGGAGCTGGCTCCAGGCCCCAGGATACACCG 2280
DB 2221 CCAGGGAAAGAAAGGGAGAGGTGGCGGGGAGCTGGCTCCAGGCCCCAGGATACACCG 2280
QY 2281 AGGAAATTAGTTGTCTGTGCTGTCTCCCTTCTCCAGTGTGAACTTCCCTTCCCTA 2340
DB 2281 AGGAAATTAGTTGTCTGTGCTGTCTCCCTTCTCCAGTGTGAACTTCCCTTCCCTA 2340
QY 2341 TCCAGGGCTCTCCCTTGTCTCTCCCTTCTCCCTTCTCCCTTCTCCCTTCTCCCTT 2400
DB 2341 TCCAGGGCTCTCCCTTGTCTCTCCCTTCTCCCTTCTCCCTTCTCCCTTCTCCCTT 2400
QY 2401 TCCCTGGGCCAGCGCTCCCGAGGGTGGAAAGGGCTCTCCCTTCTCCCTTCTCCCT 2460
DB 2401 TCCCTGGGCCAGCGCTCCCGAGGGTGGAAAGGGCTCTCCCTTCTCCCTTCTCCCT 2460
QY 2461 ATGCTGTCTTCATAGACCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2520
DB 2461 ATGCTGTCTTCATAGACCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2520
QY 2521 CTGCAACCT 2580
DB 2521 CTGCAACCT 2580
QY 2581 TCCCGAGCCCT 2640
DB 2581 TCCCGAGCCCT 2640
QY 2641 ATGGGCCACT 2700
DB 2641 ATGGGCCACT 2700
QY 2701 CCCT 2760
DB 2701 CCCT 2760
QY 2761 GTGGTCTACAGCT 2820
DB 2761 GTGGTCTACAGCT 2820
QY 2821 TCTGGCTTCCAGGGCCAGCAATGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2880
DB 2821 TCTGGCTTCCAGGGCCAGCAATGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2880
QY 2881 CCGAGCAGTGTGTGAAGGCT 2940
DB 2881 CCGAGCAGTGTGTGAAGGCT 2940
QY 2941 CGCTGCTCCCT 3000
DB 2941 CGCTGCTCCCT 3000

QY 3001 CCTCTCCAGCTCTCCAGGCT 3060
DB 3001 CCTCTCCAGCTCTCCAGGCT 3060
QY 3061 CCAAGGTTTCCCAACCCAGCAATCAGCAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3120
DB 3061 CCAAGGTTTCCCAACCCAGCAATCAGCAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3120
QY 3121 CTCTCTCTTTTCTAGCCCT 3180
DB 3121 CTCTCTCTTTTCTAGCCCT 3180
QY 3181 ACCTGCATACAAATGATATCTCTTATTGGAAAAAATCAGGGAGCCATGAACAAAGAGGCC 3240
DB 3181 ACCTGCATACAAATGATATCTCTTATTGGAAAAAATCAGGGAGCCATGAACAAAGAGGCC 3240
QY 3241 TAGATGGAGACAGGGCCAGTGTCAAGGGGACACAAAAAATAGAAAACTTTGGGAGCAGGTA 3300
DB 3241 TAGATGGAGACAGGGCCAGTGTCAAGGGGACACAAAAAATAGAAAACTTTGGGAGCAGGTA 3300
QY 3301 TCTCTCTTGGTGGTGAAGCAGGCTCTGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3360
DB 3301 TCTCTCTTGGTGGTGAAGCAGGCTCTGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3360
QY 3361 ACAGCTGAATACCTGGGCCCCCTTTCAAAGAGCCAGACTTCAACCTCTCCCGCCCTGGG 3420
DB 3361 ACAGCTGAATACCTGGGCCCCCTTTCAAAGAGCCAGACTTCAACCTCTCCCGCCCTGGG 3420
QY 3421 GGCAGAGACTCTGCCAGAGGCCACTTGTGACTGTGAGGTGTGGCGAGGCTCAATGACAA 3480
DB 3421 GGCAGAGACTCTGCCAGAGGCCACTTGTGACTGTGAGGTGTGGCGAGGCTCAATGACAA 3480
QY 3481 ACTGCGGCTGACCCAGAACTACAGAGCCCTACAGCCACTTCTGTGTACTTGGCTGGCCCT 3540
DB 3481 ACTGCGGCTGACCCAGAACTACAGAGCCCTACAGCCACTTCTGTGTACTTGGCTGGCCCT 3540
QY 3541 CAACCGTCTAGGCTGCACTGTGAGTGGCGGCGAGCTGTGGGCTTCTGTGACAGCCCT 3600
DB 3541 CAACCGTCTAGGCTGCACTGTGAGTGGCGGCGAGCTGTGGGCTTCTGTGACAGCCCT 3600
QY 3601 CCAGGGCTCTCTGGGAGCATTGCGGGCTCATGGAGCTCTGGGCTTCTGTGACAGCCCT 3660
DB 3601 CCAGGGCTCTCTGGGAGCATTGCGGGCTCATGGAGCTCTGGGCTTCTGTGACAGCCCT 3660
QY 3661 GCGCTGCTGGGACTGAACCCACTTGGACTCTGGCCCTGGCCAGTGTCTCTCTCTCTCTCT 3720
DB 3661 GCGCTGCTGGGACTGAACCCACTTGGACTCTGGCCCTGGCCAGTGTCTCTCTCTCTCTCT 3720
QY 3721 GAAGATGGAGGCTTCTGGCTGTGAAGGAGTGTGAGGCTGTGGCTGTGGGCTCTGGGCT 3780
DB 3721 GAAGATGGAGGCTTCTGGCTGTGAAGGAGTGTGAGGCTGTGGCTGTGGGCTCTGGGCT 3780
QY 3781 GGAATTTCAACCCGCTCAAGAAAGATGAGGCTCTCAGCAGCTGCACTCACTGCACTCT 3840
DB 3781 GGAATTTCAACCCGCTCAAGAAAGATGAGGCTCTCAGCAGCTGCACTCACTGCACTCT 3840
QY 3841 GGGGGCTCATGGCTTCTGACTTCTGACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3900
DB 3841 GGGGGCTCATGGCTTCTGACTTCTGACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3900
QY 3901 CCACTTTCTGAGAGCCAGCCCTGTATGCCAACACTGTGTGAGCCAGGAGCAGAGGCTG 3960
DB 3901 CCACTTTCTGAGAGCCAGCCCTGTATGCCAACACTGTGTGAGCCAGGAGCAGAGGCTG 3960
QY 3961 TGAGCCTCTGGCCCTTTCTGAGCCGGCTGGCGGTGTGATGCGATCAGCCCTGTCTCTCTCT 4020
DB 3961 TGAGCCTCTGGCCCTTTCTGAGCCGGCTGGCGGTGTGATGCGATCAGCCCTGTCTCTCTCTCT 4020
QY 4021 CCCACCTCCAAAGGTCTACCCAGCTGGGGAGGAGTACAGTAGGCCCTGTCTCTCTCTCTCT 4080
DB 4021 CCCACCTCCAAAGGTCTACCCAGCTGGGGAGGAGTACAGTAGGCCCTGTCTCTCTCTCTCTCT 4080
QY 4081 TTTCTACAGGAAGTATGCTCGAGGAGGTGTGAAGTGGTTTCAAGTGTGGTGTGAGAGGCGCT 4140

Db 4081 ||||| TTTCTACAGAAATCATGCTCCAGGAGTGTGAAGTGGTTTCAGGTGGTGACAGAGCCCT 4140
Qy 4141 CATGGCTCTGCTCTTCTGCTACCACTTGGCCAGTGCACCCAGCCCTCAGTGGCA 4200
Db 4141 CATGGCTCTGCTCTTCTGCTACCACTTGGCCAGTGCACCCAGCCCTCAGTGGCA 4200
Qy 4201 CATCTGGAGGCGAGGGGTTAGGGGCCACACACACATGCTTCTGGGGTGAAGCCCT 4260
Db 4201 CATCTGGAGGCGAGGGGTTAGGGGCCACACACACATGCTTCTGGGGTGAAGCCCT 4260
Qy 4261 TTGGCTGCCCACTCTCTTGGATGGTGTGCTCCCTTATCCCAAAATCACTCTATACA 4320
Db 4261 TTGGCTGCCCACTCTCTTGGATGGTGTGCTCCCTTATCCCAAAATCACTCTATACA 4320
Qy 4321 TCCAATTCAGGAAACAAACATGTTGGCAATTTACACAAAAGAGATGATTAACAGTG 4380
Db 4321 TCCAATTCAGGAAACAAACATGTTGGCAATTTACACAAAAGAGATGATTAACAGTG 4380
Qy 4381 CAGGGTTGGGCTGCTGATTTGGAGTGCCTTATAACACAGAGAAATACTGAAAGCAC 4440
Db 4381 CAGGGTTGGGCTGCTGATTTGGAGTGCCTTATAACACAGAGAAATACTGAAAGCAC 4440
Qy 4441 AGGGGCGAGGACAGACACAGACCCAGGAGTCTCCAAAGCACAGATGGCAACAAA 4500
Db 4441 AGGGGCGAGGACAGACACAGACCCAGGAGTCTCCAAAGCACAGATGGCAACAAA 4500
Qy 4501 ACCGAGCTGAGCATCAGGACCTTGGCTGCAATTTGCTCCAGTATACGGTGCCTCTTC 4560
Db 4501 ACCGAGCTGAGCATCAGGACCTTGGCTGCAATTTGCTCCAGTATACGGTGCCTCTTC 4560
Qy 4561 TCTGCCCTCTTCCAGGATATCTGTGGTGTGCGAGGCTGGGAGGGCAACATAGCCAC 4620
Db 4561 TCTGCCCTCTTCCAGGATATCTGTGGTGTGCGAGGCTGGGAGGGCAACATAGCCAC 4620
Qy 4621 ACCAGAGATTTCTGAAAGTTTACAAATGAGTATTTGGGGTGTAGGTGGAGCT 4680
Db 4621 ACCAGAGATTTCTGAAAGTTTACAAATGAGTATTTGGGGTGTAGGTGGAGCT 4680
Qy 4681 CCCAGGCTCTGCCCGAGCCCACTCATGACTCTAAGTGTGTGTTAATAT 4740
Db 4681 CCCAGGCTCTGCCCGAGCCCACTCATGACTCTAAGTGTGTGTTAATAT 4740
Qy 4741 TTATTTATTTGGAGATTTATTTATTTAGATGATATTTATTTGAGATTTCTATTTGTA 4800
Db 4741 TTATTTATTTGGAGATTTATTTATTTAGATGATATTTATTTGAGATTTCTATTTGTA 4800
Qy 4801 TTAACAAATAAATGTTGCTCCAGACTTTAGTCTCTTTGCCAGCTCACCCCTCTCG 4860
Db 4801 TTAACAAATAAATGTTGCTCCAGACTTTAGTCTCTTTGCCAGCTCACCCCTCTCG 4860
Qy 4861 TGCTCATCAGACTTTGCCACCCCTGCTCCCACTCCCTGCTTGTGCTGTGGAGCTGC 4920
Db 4861 TGCTCATCAGACTTTGCCACCCCTGCTCCCACTCCCTGCTTGTGCTGTGGAGCTGC 4920
Qy 4921 ACAGAGCTCTGGAGAGGCTCTTCTCCCGCACTGGGCGATGGGCGACCTCAGA 4980
Db 4921 ACAGAGCTCTGGAGAGGCTCTTCTCCCGCACTGGGCGATGGGCGACCTCAGA 4980
Qy 4981 CTTACCACTGCTGCTGCCACCAACCAACCCCTTGTATCCCTCAGTCTCCACACAGCTTC 5040
Db 4981 CTTACCACTGCTGCTGCCACCAACCAACCCCTTGTATCCCTCAGTCTCCACACAGCTTC 5040
Qy 5041 TGTCACCCAGGTTTCCCTCACCCACCTTTCGTAAGTCTTCTCA 5087
Db 5041 TGTCACCCAGGTTTCCCTCACCCACCTTTCGTAAGTCTTCTCA 5087

RESULT 2
ABK11648
ID ABK11648 standard; DNA; 5087 BP.
XX
AC ABK11648;

XX
DT 05-JUN-2002 (first entry)
XX
DE Human novel neurotrophic factor NNT1, genomic DNA.
XX
KW Human; ds; gene; NNT1; neurotrophic factor; IgE-related disease;
KW Type I allergic disease; allergic rhinitis; eczema; dermatitis;
KW pollinosis; asthma; immune disease; cancer; arteriosclerosis;
KW vascular restenosis; rheumatoid arthritis; psoriatic arthritis;
KW inflammatory arthritis; osteoarthritis; inflammatory joint disease;
KW autoimmune disease; multiple sclerosis; lupus; diabetes; endometriosis;
KW inflammatory bowel disease; transplant rejection; reproductive disorder;
KW graft versus host disease; infertility; miscarriage; preterm labour.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT misc_feature 137..138
FT /*tag= a
FT /note= "Intervening, unsequenced region of more than 1KB"
XX
XX WO200215977-A2.
XX
XX 28-FEB-2002.
XX
XX 17-AUG-2001; 2001WO-US025906.
XX
XX 18-AUG-2000; 2000US-0226436P.
XX
XX 16-AUG-2001; 2001US-00931704.
XX
XX (AMGE-) AMGEN INC.
XX
XX Senaldi G;
XX
XX WPI; 2002-280867/32.
XX
XX Treating Immunoglobulin E-related disease, modulating IgE levels in a
XX patient, preventing IgE-related disease and treating allergic diseases,
XX involves administering NNT-1 inhibitor to a patient.
XX
XX Claim 2; Fig 2; 63pp; English.
XX
XX The invention relates to treating Immunoglobulin E (IgE)-related disease,
XX modulating IgE levels in a patient, preventing an IgE-related disease,
XX and treating allergic diseases, comprising administering a
XX therapeutically effective amount of novel neurotrophic factor (NNT)-1
XX inhibitor to a patient. Also included are a method of diagnosing an IgE-
XX related disease or susceptibility to an IgE-related disease, by
XX determining the presence or amount of expression of an NNT1 polypeptide
XX encoded by a NNT1 nucleotide sequence, its fragment or naturally
XX occurring variant, and diagnosing an IgE-related disease or
XX susceptibility of an IgE-related disease based on the presence or amount
XX of expression of the polypeptide and a pharmaceutical composition for use
XX in treating IgE-related disease, comprising the NNT1 inhibitor. The NNT1
XX inhibitor is useful for preventing and treating IgE-related disease,
XX modulating IgE levels, and treating allergic diseases e.g. Type I
XX allergic disease, allergic rhinitis, eczema, dermatitis, pollinosis,
XX asthma, immune diseases and disorders, diseases involving abnormal cell
XX proliferation including cancer, arteriosclerosis and vascular restenosis,
XX diseases and conditions relating to dysfunction of immune system
XX including rheumatoid arthritis, psoriatic arthritis, inflammatory
XX arthritis, osteoarthritis, inflammatory joint disease, autoimmune
XX disease, multiple sclerosis, lupus, diabetes, inflammatory bowel disease,
XX transplant rejection, and graft versus host disease, and reproductive
XX diseases and disorders including infertility, miscarriage, preterm labour
XX and delivery, and endometriosis. The present sequence is the genomic DNA
XX for human NNT1
XX
XX Sequence 5087 BP; 992 A; 1746 C; 1191 G; 1158 T; 0 U; 0 Other;

Query Match 100.0%; Score 5087; DB 6; Length 5087;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5087; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4381 CAGGGTTGGGCTGCAATTGAGGTGCCCTATAAACCCAGAGAGAAAAATCTGAAGCAC 4440
 Db 4381 CAGGGTTGGGCTGCAATTGAGGTGCCCTATAAACCCAGAGAGAAAAATCTGAAGCAC 4440
 QY 4441 AGGGGACAGGACACAGACAGACAGACAGAGTCTCCAAAGACACAGAGTGGCAACAAA 4500
 Db 4441 AGGGGACAGGACACAGACAGACAGAGTCTCCAAAGACACAGAGTGGCAACAAA 4500
 QY 4501 ACCGAGCTGAGCATCAGGACCTTGCCTCGAATGTCTTCCAGTATTACGGTCTCTTC 4560
 Db 4501 ACCGAGCTGAGCATCAGGACCTTGCCTCGAATGTCTTCCAGTATTACGGTCTCTTC 4560
 QY 4561 TCTCCCCCTTCCAGGATCTGTGGTTCAGAGTGGGAGGACCAACCATAGCAC 4620
 Db 4561 TCTCCCCCTTCCAGGATCTGTGGTTCAGAGTGGGAGGACCAACCATAGCAC 4620
 QY 4621 ACCAGAGATTCTCTGAAAGTTTACAATGCAGTAGCATTTTGGGGTGTAGGGTGGCAGCT 4680
 Db 4621 ACCAGAGATTCTCTGAAAGTTTACAATGCAGTAGCATTTTGGGGTGTAGGGTGGCAGCT 4680
 QY 4681 CCCAAGCCCTGCCCCAGCCACCCAGCTATGACTCTAAGTGTGTGTTATATAT 4740
 Db 4681 CCCAAGCCCTGCCCCAGCCACCCAGCTATGACTCTAAGTGTGTGTTATATAT 4740
 QY 4741 TTATTTATTTGGAGATGTTATTTATTTAGATGATATTTATTGCAGATTTCTATTCTTGTA 4800
 Db 4741 TTATTTATTTGGAGATGTTATTTATTTAGATGATATTTATTGCAGATTTCTATTCTTGTA 4800
 QY 4801 TTAACAAATAAATGCTTGGCCAGAACTTAGTCTCTTTGGCCAGCCTCAACCCCTCTGG 4860
 Db 4801 TTAACAAATAAATGCTTGGCCAGAACTTAGTCTCTTTGGCCAGCCTCAACCCCTCTGG 4860
 QY 4861 TGCTCATCAGACTCTTGCCACCCCTGGCTCCCACTCCCTGCTGCTCTGCTGAGCTGC 4920
 Db 4861 TGCTCATCAGACTCTTGCCACCCCTGGCTCCCACTCCCTGCTGCTCTGCTGAGCTGC 4920
 QY 4921 ACAGAGCTCTGGGAAGAGGCCCTCTTCTCCCTCCGCACTGGGGCGATGGGGCACTCAGA 4980
 Db 4921 ACAGAGCTCTGGGAAGAGGCCCTCTTCTCCCTCCGCACTGGGGCGATGGGGCACTCAGA 4980
 QY 4981 CTTACCCACTGCTGTCACACACACACACCCCTTATGCTCAGTCTCCACACAGCTTC 5040
 Db 4981 CTTACCCACTGCTGTCACACACACACACCCCTTATGCTCAGTCTCCACACAGCTTC 5040
 QY 5041 TGTCCACCCAGGTTTCCCTCACCCACCTTTGCTAAGTCTTCTCA 5087
 Db 5041 TGTCCACCCAGGTTTCCCTCACCCACCTTTGCTAAGTCTTCTCA 5087

RESULT 3

AAV22653 standard; DNA; 5088 BP.

XX AAV22653;

XX 13-JUL-1998 (first entry)

XX Human genomic DNA encoding neurotrophic factor NNT-1.

XX Human; neurotrophic factor; NNT-1; growth; motor; sympathetic; neuron;

XX treatment; neurological disease; degeneration; Parkinson's disease;

XX amyotrophic lateral sclerosis; ALS; Alzheimer's disease; stroke; ss.

XX Homo sapiens.

OS Key Location/Qualifiers

FH misc_feature 138

FT /tag= a

FT /note= "represents intervening unsequenced region of 1

FT Kb"

XX US5741772-A.

XX 21-APR-1998.
 PD 03-FEB-1997; 97US-00792019.
 PF 03-FEB-1997; 97US-00792019.
 PR 03-FEB-1997; 97US-00792019.
 PX (AMGE-) AMGEN INC.
 PA Chang M;
 PI WPI; 1998-260526/23.
 DR Neurotrophic factor NNT-1 polypeptide and related nucleic acids - useful
 PT for stimulating growth of motor and sympathetic neurons.
 PS Disclosure; Fig 2; 41pp; English.
 XX The present sequence encodes a human neurotrophic factor, designated NNT-
 CC 1, which is capable of stimulating growth of motor or sympathetic
 CC neurons. The NNT-1 protein is useful in the treatment of neurological
 CC diseases characterised by the degeneration and death of particular
 CC classes of neurons. These diseases specifically include Parkinson's
 CC disease, amyotrophic lateral sclerosis (ALS), Alzheimer's disease, stroke
 CC and various degenerative disorders affecting vision
 XX Sequence 5088 BP; 992 A; 1746 C; 1191 G; 1158 T; 0 U; 1 Other;

Query Match 99.8%; Score 5076; DB 2; Length 5088;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 5087; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 AACCTCGAGTGGGCTGGCGATGGGATTATTAAGCTTCGCGAGCGCGGCTCGCC 60
 Db 1 AACCTCGAGTGGGCTGGCGATGGGATTATTAAGCTTCGCGAGCGCGGCTCGCC 60
 QY 61 CTCCTACTCGGACGCTCCGGAGAGGAGCGCACCCGGCGGCGCCAGCCGCCA 120
 Db 61 CTCCTACTCGGACGCTCCGGAGAGGAGCGCACCCGGCGGCGCCAGCCGCCA 120
 QY 121 TGGACCTCCGAGCAGGT-TGAAACCCAACTAGCCCTGCTCTTATACATGACAAGA 179
 Db 121 TGGACCTCCGAGCAGGT-TGAAACCCAACTAGCCCTGCTCTTATACATGACAAGA 180
 QY 180 GGGCCCATCTGATACCTAAACCGACCAAGTACAGCCCTCCAACTCACCCTCTGCCTGC 239
 Db 181 GGGCCCATCTGATACCTAAACCGACCAAGTACAGCCCTCCAACTCACCCTCTGCCTGC 240
 QY 240 CGAGACTCACCACATCTCTTGGACTCAAACTCAACCGCACTAAATCAACCAATGCC 299
 Db 241 CGAGACTCACCACATCTCTTGGACTCAAACTCAACCGCACTAAATCAACCAATGCC 300
 QY 300 AAGTCTAAACTAATCTGAAACTTTTAAAGTAAACCCAGTCTTAAACCTAACCTAGCCCAA 359
 Db 301 AAGTCTAAACTAATCTGAAACTTTTAAAGTAAACCCAGTCTTAAACCTAACCTAGCCCAA 360
 QY 360 TGCCAATTATCTACCTAGCCAAACCTAATCTGCTTTGGCAGTCCAAAGTGCCACT 419
 Db 361 TGCCAATTATCTACCTAGCCAAACCTAATCTGCTTTGGCAGTCCAAAGTGCCACT 420
 QY 420 GAATCTCACTTGGTCTCCTCAGTGAATAATCCAGAAAAGCATATTTCCCACTGCCCA 479
 Db 421 GAATCTCACTTGGTCTCCTCAGTGAATAATCCAGAAAAGCATATTTCCCACTGCCCA 480
 QY 480 TCCCTCTTTACAGCACCCAAACCTCTGCTCTGGACTCTGGTATCTGGGATGTCCAAAC 539
 Db 481 TCCCTCTTTACAGCACCCAAACCTCTGCTCTGGACTCTGGTATCTGGGATGTCCAAAC 540
 QY 540 TCTGCGATGCCATCAGCCAAAGCCGACTCGTGAATGCACTCTCTCCCTCTCTGTC 599
 Db 541 TCTGCGATGCCATCAGCCAAAGCCGACTCGTGAATGCACTCTCTCCCTCTCTGTC 600
 QY 600 CCACACCTTGCAGGCTGATGGAAAGGCGCTCAATTGAAGTCCAACTTTTCCCACTAACAC 659

Db 601 |||||CCACCC|||TGAGGCTGATGGAAGGCTCATTGAAGTCCAACCTTTCCCACTTAACAC 660
QY 660 |||||CAAGAACGGGTGAACCTCGACACTGCGACCGTTCCTGAGAGTGAAGCTAAATCTCTCT 719
Db 661 |||||CAAGAACGGGTGAACCTCGACACTGCGACCGTTCCTGAGAGTGAAGCTAAATCTCTCT 720
QY 720 |||||TCAATCTAACCCCACTCACTTCCACACTCAGGAATCACATCCTAGAAATATACCCAA 779
Db 721 |||||TCAATCTAACCCCACTCACTTCCACACTCAGGAATCACATCCTAGAAATATACCCAA 780
QY 780 |||||AATTAAGCCCATTAAGGACGCGACCTTAGTGGTCTAAACCTTAACCTTGTCTCTATG 839
Db 781 |||||AATTAAGCCCATTAAGGACGCGACCTTAGTGGTCTAAACCTTAACCTTGTCTCTATG 840
QY 840 |||||GGTGAAGTCTGTTCTTGGCGCGCGCTCTCTCTGCTTCTCTCTAGAGCTGACTGTCT 899
Db 841 |||||GGTGAAGTCTGTTCTTGGCGCGCGCTCTCTCTGCTTCTCTCTAGAGCTGACTGTCT 900
QY 900 |||||CAGCTGCCAGCTCTGACATGTCTCTTCCACCTCTGACTCCCTCAAGCTGCACTG 959
Db 901 |||||CAGCTGCCAGCTCTGACATGTCTCTTCCACCTCTGACTCCCTCAAGCTGCACTG 960
QY 960 |||||GGACTGGAGACTGGCAGGAAGCTAGGTACAACTGGAACACAGCAGCTGACCTGCAG 1019
Db 961 |||||GGACTGGAGACTGGCAGGAAGCTAGGTACAACTGGAACACAGCAGCTGACCTGCAG 1020
QY 1020 |||||TCCCTAGGCTTGCCCGCGCTCCCTCCATGTACACATATACATATACATATACATAT 1079
Db 1021 |||||TCCCTAGGCTTGCCCGCGCTCCCTCCATGTACACATATACATATACATATACAT 1080
QY 1080 |||||GGCACAATGCGAAAGCTCTCTCAGCTGACACACAGATCCATTTCAAGTATCTACTGA 1139
Db 1081 |||||GGCACAATGCGAAAGCTCTCTCAGCTGACACACAGATCCATTTCAAGTATCTACTGA 1140
QY 1140 |||||TAGACACTCATGGTGCCCAAGTCTCATCTCAACATACATACATCTCTCTCTCTCTCC 1199
Db 1141 |||||TAGACACTCATGGTGCCCAAGTCTCATCTCAACATACATACATCTCTCTCTCTCTCC 1200
QY 1200 |||||CGTCTTGCCAGAGTGTTCCTCCCTCTCCATCCCTCTGCTCCCTCCATCTGCTGCTCC 1259
Db 1201 |||||CGTCTTGCCAGAGTGTTCCTCCCTCTCCATCCCTCTGCTCCCTCCATCTGCTGCTCC 1260
QY 1260 |||||CTCACCCCCCACTCAGCTGGGACAGACCTGAGGCTGCCAGCTGCTCTCC 1319
Db 1261 |||||CTCACCCCCCACTCAGCTGGGACAGACCTGAGGCTGCCAGCTGCTCTCC 1320
QY 1320 |||||CGTGTGGGCGCGCGCTCATGCTTCTCGTCCATCTGCTCCCACTGAGGACTCGTGG 1379
Db 1321 |||||CGTGTGGGCGCGCGCTCATGCTTCTCGTCCATCTGCTCCCACTGAGGACTCGTGG 1380
QY 1380 |||||GGATGTTAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1439
Db 1381 |||||GGATGTTAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
QY 1440 |||||GCACAGGACCCAGGCTGCGCTCCATCCAGAAACCTATGAGCTCAACCTGCTTACC 1499
Db 1441 |||||GCACAGGACCCAGGCTGCGCTCCATCCAGAAACCTATGAGCTCAACCTGCTTACC 1500
QY 1500 |||||TGGAGACCAATCCCGAGCTGGTGGGACCTATGTGAGTATCCAGCTGAGGAATCTGG 1559
Db 1501 |||||TGGAGACCAATCCCGAGCTGGTGGGACCTATGTGAGTATCCAGCTGAGGAATCTGG 1560
QY 1560 |||||GAGTGGGAGGAGTGAAGTGGGAAAGCAGTCTTAACCTGGAAGGCTTCTGGTAA 1619
Db 1561 |||||GAGTGGGAGGAGTGAAGTGGGAAAGCAGTCTTAACCTGGAAGGCTTCTGGTAA 1620
QY 1620 |||||ATGATGGGTGAGGAGGAGCTTGGCTCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1679
Db 1621 |||||ATGATGGGTGAGGAGGAGCTTGGCTCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680
QY 1680 |||||GCCCTTCCCTCTAGGTGGCGCGCGCTTCCCATCCCTGCGCCCGAGGACTGAGCATGT 1739

Db 1681 |||||GCCCTTCCCTCTAGGTGGCGCGCGCGCTTCCCATCCCTGCGCCCGAGGACTAGCATGT 1740
QY 1740 |||||GGGAGAGCTCGCACCGCGCTTGCGCATTTGCGCCCTGCTGCTGCTGCTGCTGCTGCTGCT 1799
Db 1741 |||||GGGAGAGCTCGCACCGCGCTTGCGCATTTGCGCCCTGCTGCTGCTGCTGCTGCTGCTGCT 1800
QY 1800 |||||CTCCCCCTGGGGCGCGGGGAAGTCTCTCTGTTTACACCTGTTGTGGTGTCTCTTGGCG 1859
Db 1801 |||||CTCCCCCTGGGGCGCGGGGAAGTCTCTCTGTTTACACCTGTTGTGGTGTCTCTTGGCG 1860
QY 1860 |||||GGGCGGGTGGTGGGGAAGAGGCGCCCACTGCCATGCCCTGGTTCAGCTGCGCT 1919
Db 1861 |||||GGGCGGGTGGTGGGGAAGAGGCGCCCACTGCCATGCCCTGGTTCAGCTGCGCT 1920
QY 1920 |||||CTGCCCCAGACCTGGGGCGCTCTGCTCTGGAACCCAGGGGCGCTCTCTCTGCTCTGCTCT 1979
Db 1921 |||||CTGCCCCAGACCTGGGGCGCTCTGCTCTGGAACCCAGGGGCGCTCTCTCTGCTCTGCTCT 1980
QY 1980 |||||TCCATCTAGCTGGGCTCTTAGGGGGTCTAGGGGGAAGGGGACTGTAGGGAACCCAG 2039
Db 1981 |||||TCCATCTAGCTGGGCTCTTAGGGGGTCTAGGGGGAAGGGGACTGTAGGGAACCCAG 2040
QY 2040 |||||GCAGTAGTGGCAGGGGTTTAGGGTGTGAGGTATGCTGTAAGGATTTGGGGGTG 2099
Db 2041 |||||GCAGTAGTGGCAGGGGTTTAGGGTGTGAGGTATGCTGTAAGGATTTGGGGGTG 2100
QY 2100 |||||GTCCAGAGGTGTTTACAGAGCCCGAGAGAAAGAGGGTGGAGGAGCGAGGAC 2159
Db 2101 |||||GTCCAGAGGTGTTTACAGAGCCCGAGAGAAAGAGGGTGGAGGAGCGAGGAC 2160
QY 2160 |||||CATGGGAAACCGCGCGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2219
Db 2161 |||||CATGGGAAACCGCGCGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2220
QY 2220 |||||GCCAGGAAAGAAAGAGGAGAGGTGGGGGAGCTGCTCAGCCCGAGGATACAC 2279
Db 2221 |||||GCCAGGAAAGAAAGAGGAGAGGTGGGGGAGCTGCTCAGCCCGAGGATACAC 2280
QY 2280 |||||GAGGAATAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2339
Db 2281 |||||GAGGAATAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2340
QY 2340 |||||ATCCAGGCTCTCCCGCT 2399
Db 2341 |||||ATCCAGGCTCTCTCCCGCT 2400
QY 2400 |||||TTCCCTGGGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2459
Db 2401 |||||TTCCCTGGGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2460
QY 2460 |||||CATGCTGCTCTCATAGCTTCT 2519
Db 2461 |||||CATGCTGCTCTCATAGCTTCT 2520
QY 2520 |||||TCTGCAACCTGCT 2579
Db 2521 |||||TCTGCAACCTGCT 2580
QY 2580 |||||CTCCCCAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2639
Db 2581 |||||CTCCCCAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2640
QY 2640 |||||AATGGGCACTCTCATCT 2699
Db 2641 |||||AATGGGCACTCTCATCT 2700
QY 2700 |||||GCCCTCTAGTTCGCGACCTTTCT 2759
Db 2701 |||||GCCCTCTAGTTCGCGACCTTTCT 2760
QY 2760 |||||AGTGGTACACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2819
Db 2761 |||||AGTGGTACACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2820

Db 4981 ACTTACCACTGCTGTCACCAACCAACCCCTTGATCCCTCAGTCCCTCCACAGCTT 5040
QY 5040 CTGTCACCCAGGTTTCCTCACCACCTTTGCTTAAGTCTTCTCTCA 5087
Db 5041 CTGTCACCCAGGTTTCCTCACCACCTTTGCTTAAGTCTTCTCTCA 5088

RESULT 4
ID AAV47511 standard; cDNA; 5088 BP.
XX AAV47511;
AC AAV47511;
XX 09-NOV-1998 (first entry)
XX Human neurotrophic factor NNT-1 genomic DNA.
XX NNT-1; neurotrophic factor; human; antiinflammatory; adjuvant;
KW Alzheimer's disease; Parkinson's disease; Huntington's disease;
KW amyotrophic lateral sclerosis; Charcot-Marie-Tooth syndrome;
KW peripheral neuropathy; dystrophy; neural retina degeneration;
KW common variable immunodeficiency; CVID; selective IgA deficiency;
KW hypogammaglobulinaemia; X-linked agammaglobulinaemia; antiseptic;
KW therapy; ss.
XX Homo sapiens.
XX

Location/Qualifiers
FH Key 1. .119
FT 5'UTR /*tag= a
FT CDS 120..3857
FT /*tag= b
FT /*note= "contains 2 introns"
FT exon 120..135
FT /*tag= c
FT /*number= 1
FT intron 136..1368
FT /*tag= d
FT /*number= 1
FT misc_feature 137..138
FT /*tag= e
FT /*note= "intervening unsequenced region of >1kb"
FT exon 1369..1535
FT /*tag= f
FT intron 1536..3365
FT /*tag= g
FT /*number= 2
FT exon 3366..3857
FT /*tag= h
FT /*number= 3

WO9833922-A1.
XX
XX 06-AUG-1998.
XX
XX 02-FEB-1998; 98WO-US002363.
XX
XX 03-FEB-1997; 97US-00792019.
XX 30-JAN-1998; 98US-00016534.
XX
XX (AMGE-) AMGEN INC.
XX
XX Chang M, Elliot GS, Senaldi G, Sarmiento U;
XX WPI; 1998-437475/37.
XX P-PSDB; AAW29715.
XX
XX Newly isolated nucleic acid encoding human or murine neurotrophic factor
XX NNT-1 - useful for treatment of neurological and immunological diseases
XX or inflammation, also as vaccine adjuvant.
XX

PS This newly isolated human genomic DNA sequence (deposited at ATCC 98294)
XX codes for a novel neurotrophic factor, designated NNT-1 (see AAW29715),
CC that is a growth factor for neurons and for B or T cells. It was obtained
CC from a human genomic pl library using human NNT-1 cDNA (see AAV47510) as
CC probe. Vectors containing the cDNA or genomic DNA and host cells are
CC provided for use in the production of NNT-1 polypeptides. These are used
CC to treat: (i) neurological or immunological diseases, specifically
CC Alzheimer's, Parkinson's or Huntington's diseases, amyotrophic lateral
CC sclerosis, Charcot-Marie-Tooth syndrome, peripheral neuropathy, dystrophy
CC and degeneration of the neural retina, or conditions characterised by T
CC or B cell defects, e.g. common variable immunodeficiency (CVID),
CC selective IgA deficiency, hypogammaglobulinaemia and X-linked
CC agammaglobulinaemia (claimed), but many others disclosed; and (ii)
CC inflammation. NNT-1 is also able to boost immunoreactivity and antibody
CC production following vaccination, and, since it inhibits tumour necrosis
CC factor production, it may also be useful for treating sepsis. NNT-1
CC nucleic acid fragments are also used as hybridisation probes in
CC diagnostic assays. In addition, cells that have been engineered to
CC express NNT-1 can be implanted, or nucleic acids are delivered in gene
XX therapy vectors
SQ Sequence 5088 BP; 992 A; 1746 C; 1191 G; 1158 T; 0 U; 1 Other;

Query Match 99.8%; Score 5076; DB 2; Length 5088;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5087; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 AACCTGCGAGTGGGCTTGGCGGATGGGATTTAAAGCTTTCGCGGAGCGCGCTCGCC 60
Db 1 AACCTGCGAGTGGGCTTGGCGGATGGGATTTAAAGCTTTCGCGGAGCGCGCTCGCC 60

QY 61 CTCCTCACTCCGAGCTCCGCGGAGGAGCCGACCCGCGCGCGCCAGCCGCCA 120
Db 61 CTCCTCACTCCGCGGAGCTCCGCGGAGGAGCCGACCCGCGCGCGCCAGCCGCCA 120

QY 121 TGGACCTCCGAGGAGTTGAAAACCCAACTAGCCCTGCTTTTATAACATGACAGCAG 180
Db 121 TGGACCTCCGAGGAGTTGAAAACCCAACTAGCCCTGCTTTTATAACATGACAGCAG 180

QY 181 CGCCCCATCTGATACCTAAACCGACCAAGTCACAGCCCTCAACTGCTGCTGCTGCC 240
Db 181 CGCCCCATCTGATACCTAAACCGACCAAGTCACAGCCCTCAACTGCTGCTGCTGCC 240

QY 241 CAGACCTCAGACATCCTTG-TGAGCTCAAACTCAACCCGACCTAAATCAACCAATCCC 299
Db 241 CAGACCTCAGACATCCTTG-TGAGCTCAAACTCAACCCGACCTAAATCAACCAATCCC 300

QY 300 AAGTCTAAACTAATCTGAAACTTTTAAAGTAACCCAGTCTTTAAACCTAGGCCCAA 359
Db 301 AAGTCTAAACTAATCTGAAACTTTTAAAGTAACCCAGTCTTTAAACCTAGGCCCAA 360

QY 360 TGCCAATTATATCTACCTAGCCAAACCCCTAAGTCTTTCGAGTCCCAAGTGTCCACT 419
Db 361 TGCCAATTATATCTACCTAGCCAAACCCCTAAGTCTTTCGAGTCCCAAGTGTCCACT 420

QY 420 GAATCTCTACCTGGTCTCTCACTGAAAATCCGAGAAAAGCATATTTCCCACTGCCACA 479
Db 421 GAATCTCTACCTGGTCTCTCACTGAAAATCCGAGAAAAGCATATTTCCCACTGCCACA 480

QY 480 TCCCTCCTTACAGCACCACCCCTGCGCTCTGAGCTCTCTGGTATCTTGGATGTCCAAAC 539
Db 481 TCCCTCCTTACAGCACCACCCCTGCGCTCTGAGCTCTCTGGTATCTTGGATGTCCAAAC 540

QY 540 TCTGAGTGCATCAGCCAAACAGCCCGAGTCTCTGAAATGCACTCTCTCCCTCTCTGTC 599
Db 541 TCTGAGTGCATCAGCCAAACAGCCCGAGTCTCTGAAATGCACTCTCTCTCCCTCTCTGTC 600

QY 600 CCCACCTTTCAGGCTGATGGAAGGCTCATTTGAAGTCCCACTTTTCCCACTAACAC 659
Db 601 CCCACCTTTCAGGCTGATGGAAGGCTCATTTGAAGTCCCACTTTTCCCACTAACAC 660

Qy	660	CAAGAACGGGGTGAACCTCCACACTGCCACGGTTCCCTGAGAGTGAGCACTAAATCTCCT	719
Db	661	CAAGAACGGGGTGAACCTCCACACTGCCACGGTTCCCTGAGAGTGAGCACTAAATCTCCT	720
Qy	720	TCAAATCTAACCCCCACACCTACACTTCCACACTCAGGAATCACATCTCTAGAAATATACCCAA	779
Db	721	TCAAATCTAACCCCCACACCTACACTTCCACACTCAGGAATCACATCTCTAGAAATATACCCAA	780
Qy	780	AACCTAAGCCCCATAAGCAGCCCGACCTAGTGGTCTAAACCTATATACCTTGCCTTCCTATG	839
Db	781	AACCTAAGCCCCATAAGCAGCCCGACCTAGTGGTCTAAACCTATATACCTTGCCTTCCTATG	840
Qy	840	GGTGAGTCTGTTCTTGGCGCGCCTCTCTCCCTGCTTCTCCCTTAGAGCTGACTGTGCT	899
Db	841	GGTGAGTCTGTTCTTGGCGCGCCTCTCTCCCTGCTTCTCCCTTAGAGCTGACTGTGCT	900
Qy	900	CAGCCTGCCAGCTCTGACATGTGTGTCTCCCAACCTCTGACTCCCTCAAGCTGCAGTG	959
Db	901	CAGCCTGCCAGCTCTGACATGTGTGTCTCCCAACCTCTGACTCCCTCAAGCTGCAGTG	960
Qy	960	GGACTGGAAGACTGGCAGGAAGCTAGGGTACAACCTGGAAACACAGGCAGGTGCACTTCGAG	1019
Db	961	GGACTGGAAGACTGGCAGGAAGCTAGGGTACAACCTGGAAACACAGGCAGGTGCACTTCGAG	1020
Qy	1020	TCCCTAGGCTGGCCCCGTCCCTCCATGTATACACATATACATGTGGCACACACACAGT	1079
Db	1021	TCCCTAGGCTGGCCCCGTCCCTCCATGTATACACATATACATGTGGCACACACACAGT	1080
Qy	1080	GGCACATATGCCAAAGACTCTCTCAGGTGACACACAGATCCATCTCAAGATATCTACTGA	1139
Db	1081	GGCACATATGCCAAAGACTCTCTCAGGTGACACACAGATCCATCTCAAGATATCTACTGA	1140
Qy	1140	TAGACACTCATCGTGTGCAAGTCTCATCTCAAAATACACATGCTCTCTTTCTCTCC	1199
Db	1141	TAGACACTCATCGTGTGCAAGTCTCATCTCAAAATACACATGCTCTCTTTCTCTCC	1200
Qy	1200	CGTCTTGCCAGGAGTGTTCCTCCTCTCCATCCCTCTGCTGCCATCTGGTGTCCCAAC	1259
Db	1201	CGTCTTGCCAGGAGTGTTCCTCCTCTCCATCCCTCTGCTGCCATCTGGTGTCCCAAC	1260
Qy	1260	CTCACCCCCACCCAGCCCAAGTGGGGACAGACACTGAGGGGCTGCCAGCTGCTTCCC	1319
Db	1361	CTCACCCCCACCCAGCCCAAGTGGGGACAGACACTGAGGGGCTGCCAGCTGCTTCCC	1320
Qy	1320	CGTGTGGGCCCCGGCCCGGTCTATCTTCGTCCATCTCTGCCACAGGGGACTCGTGGG	1379
Db	1321	CGTGTGGGCCCCGGCCCGGTCTATCTTCGTCCATCTCTGCCACAGGGGACTCGTGGG	1380
Qy	1380	GGATGTTAGCGTGTCTGTGCAGGTGTCTTGCGACCTTCCCTGCAGTGCCAGCTCTCAATC	1439
Db	1381	GGATGTTAGCGTGTCTGTGCAGGTGTCTTGCGACCTTCCCTGCAGTGCCAGCTCTCAATC	1440
Qy	1440	GCACAGGGGACCCAGGGCCTGGCCCCCTCCATCCAGAAAACCTATGACCTCACCCGCTACC	1499
Db	1441	GCACAGGGGACCCAGGGCCTGGCCCCCTCCATCCAGAAAACCTATGACCTCACCCGCTACC	1500
Qy	1500	TGGAGCACCAACTCCGACGTTGCTGGGACCTATGTAGTATCCACGGTAGGAATCTGG	1559
Db	1501	TGGAGCACCAACTCCGACGTTGCTGGGACCTATGTAGTATCCACGGTAGGAATCTGG	1560
Qy	1560	GAGTTGGGGAGGTGAGGAGTTCGGGAAAGACAGTCTCAACCGTGAGAGGTTCTCGTAA	1619
Db	1561	GAGTTGGGGAGGTGAGGAGTTCGGGAAAGACAGTCTCAACCGTGAGAGGTTCTCGTAA	1620
Qy	1620	ATGATGGGGTGAGGAGGGCTCTTTGGCTCCACAGTCCCTCTGTGTCTATCTCCT	1679
Db	1621	ATGATGGGGTGAGGAGGGCTCTTTGGCTCCACAGTCCCTCTGTGTCTATCTCCT	1680
Qy	1680	GCCCTTCCTCTTAGTGGCCCCCCCCTATCTCCCATCTCCCTGGCCCCCAGGACTAGGCAATG	1739
Db	1681	GCCCTTCCTCTTAGTGGCCCCCCCCTATCTCCCATCTCCCTGGCCCCCAGGACTAGGCAATG	1740
Qy	1740	GGGCAGGGCCTGGCACCCCGCCTTGGCCCATTTGCCCATCTGGCTGCCAGCCAGCGCCCGC	1799

1741	GGGCAAGGCTCGCACCCCGCCTTGGCCCATTTGCCCACTGGCTGCCAGCCAGCCGCCGC	1800
1800	CTCCCCCTGGGGGCGGGGAAGTCTCTCTGTATTACACCGTGTGTGTGTCTCTTGGCG	1859
1801	CTCCCCCTGGGGGCGGGGAAGTCTCTCTGTATTACACCGTGTGTGTGTCTCTTGGCG	1860
1860	GGGCGGGTGTGGTGGGGACAGAGGGGCCACCTCCATGCTCGCTCCGTTCCAGTCCGCT	1919
1861	GGGCGGGTGTGGTGGGGACAGAGGGGCCACCTCCATGCTCGCTCCGTTCCAGTCCGCT	1920
1920	CTGCCCCAGACCTGGGGCCCTGCTGCTGGACCCAGAGGGGCTCCCTTCCGTTCTGCTC	1979
1921	CTGCCCCAGACCTGGGGCCCTGCTGCTGGACCCAGAGGGGCTCCCTTCCGTTCTGCTC	1980
1980	TCCCATCTTAGCTGGGCCCTCTAGGGGGGTCTAGGGGGTCAATGGGGAAGGGGAACCCAG	2039
1981	TCCCATCTTAGCTGGGCCCTCTAGGGGGGTCTAGGGGGTCAATGGGGAAGGGGAACCCAG	2040
2040	GCAGTAGTGGCAGGGGGTTAGGGTGTGGATGAGGTTATGCTGTAAAGATTGGGGGTG	2099
2041	GCAGTAGTGGCAGGGGGTTAGGGTGTGGATGAGGTTATGCTGTAAAGATTGGGGGTG	2100
2100	GTCCAGAGGTGTTCAGAGAGCCAGGAGAGAAGAAAGGAGGTGTGGAGAGCCGAGGCAC	2159
2101	GTCCAGAGGTGTTCAGAGAGCCAGGAGAGAAGAAAGGAGGTGTGGAGAGCCGAGGCAC	2160
2160	CATGGGAACCGGCCCTCTTCCCGTGTCTCTTCCATCCAGACCCCTACTCTCGA	2219
2161	CATGGGAACCGGCCCTCTTCCCGTGTCTCTTCCATCCAGACCCCTACTCTCGA	2220
2220	GCCAGGGAAGAAAGGAAGAGGTGGCGGGGAGCTGGCTCCAGCCCCAGGATACACC	2279
2221	GCCAGGGAAGAAAGGAAGAGGTGGCGGGGAGCTGGCTCCAGCCCCAGGATACACC	2280
2280	GAGGAATTAGTTTGTCTCTGTCTGTGACGCTGTGAACCTTCCCTGGGCCCTTGCT	2339
2281	GAGGAATTAGTTTGTCTCTGTGCTGTGACGCTGTGAACCTTCCCTGGGCCCTTGCT	2340
2340	ATCCCAGGCGCTCCCTTGTCTCTCCCTCTCTTTCACAGTTATACATCTCCCTCATCCCT	2399
2341	ATCCCAGGCGCTCCCTTGTCTCTCCCTCTCTTTCACAGTTATACATCTCCCTCATCCCT	2400
2400	TTCCTTGGGCCCGAGCGCTCCCCGAGGGTTGGAAGGGCTCTGCCCTCTTCCCTATAC	2459
2401	TTCCTTGGGCCCGAGCGCTCCCCGAGGGTTGGAAGGGCTCTGCCCTCTTCCCTATAC	2460
2460	CATGCTGTCTTCATAGCTTCTCTCTGTCTACTCATGAGACTGCTCCATTCTCTCT	2519
2461	CATGCTGTCTTCATAGCTTCTCTCTGTCTACTCATGAGACTGCTCCATTCTCTCT	2520
2520	TCTGCAACCTCGCTCTATAGCTGAACCTTCTTTGGAGTGTAGTGAGTACCCGCT	2579
2521	TCTGCAACCTCGCTCTATAGCTGAACCTTCTTTGGAGTGTAGTGAGTACCCGCT	2580
2580	CTCCCGAGCCCTCAGCTGTGGCGCTGGGTGTGACGGGAAATGGGGCTCTGTTCC	2639
2581	CTCCCGAGCCCTCAGCTGTGGCGCTGGGTGTGACGGGAAATGGGGCTCTGTTCC	2640
2640	AATGGGCCACTCTCATCTCTCTCTTGTTCCTGTGCGAGAAACCTTGTCTTCACTCCACT	2699
2641	AATGGGCCACTCTCATCTCTCTCTTGTTCCTGTGCGAGAAACCTTGTCTTCACTCCACT	2700
2700	GCCTCTCTAGTTCGGACCTTTTCTCTCTGGCTTTCCTGCGCAATTTCTCCAGG	2759
2701	GCCTCTCTAGTTCGGACCTTTTCTCTCTGGCTTTCCTGCGCAATTTCTCCAGG	2760
2760	AGTGTCTACACCTCTGCCTCCACTTCTCTCCACCACTCACTTCTTAAACCCCTGCA	2819
2761	AGTGTCTACACCTCTGCCTCCACTTCTCTCCACCACTCACTTCTTAAACCCCTGCA	2820
2820	ATCTGGCTTCCAGGCCCGAGAAATGTTTCTCTCCAGGCTGTGAGGCACCTCTTGCCTAA	2879

Db 2821 ATCTGCTCTCCAGGCCCCAGCAATGGTCTCTCCAAAGGTCGTGAGCAGCCTCTCTTGCCAA 2880
Qy 2880 GCCCGACAGTGTTTTGAAGGCTCATCTCTCTGCTGCTCTGTTTGGAGGACCACTGCTGA 2939
Db 2881 GCCCGACAGTGTTTGAGGGCTCATCTCTCTGCTGCTGTTTGGAGGACCACTGCTGA 2940
Qy 2940 GCGCTGTGCTCTCTCGAATCTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2999
Db 2941 GCGCTGTGCTCTCTCGAATCTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3000
Qy 3000 ACCTCTCCAGCTCTCTCCAGGCTCTCTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3059
Db 3001 ACCTCTCCAGCTCTCTCCAGGCTCTCTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3060
Qy 3060 CCCAAGGTTTGGCCACCCAGCCCAATCAGACGCTCTCTCTCTCTGCTGCTGCTGCTGCTGCTGCT 3119
Db 3061 CCCAAGGTTTGGCCACCCAGCCCAATCAGACGCTCTCTCTCTCTGCTGCTGCTGCTGCTGCTGCT 3120
Qy 3120 CTTCT 3179
Db 3121 CTTCT 3180
Qy 3180 CACTCTCATCAATATATCTCTTATTGGAAGAACTCAGGAGGCTCAGCAAGGAAAGC 3239
Db 3181 CACTCTCATCAATATATCTCTTATTGGAAGAACTCAGGAGGCTCAGCAAGGAAAGC 3240
Qy 3240 CTAGCATGAGACAGGCGCAGTGTGAGGGACACAAATAAGAACTTTGGAGCAGGT 3299
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Qy 3300 ATCTCTCTGCTGTGAGCAGGCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3359
Db 3301 ATCTCTCTGCTGTGAGCAGGCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3360
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Db 3361 CACAGTGAATACCTTGGGCCCCCTTTCAAGAGCCAGACTTCAACCTCTCCCGCTGG 3420
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Qy 3480 AACTGGGCTGACCCAGAACTAGAGGCTCAGCCACCTCTCTGTTACTTGGCTGGCC 3539
Db 3481 AACTGGGCTGACCCAGAACTAGAGGCTCAGCCACCTCTCTGTTACTTGGCTGGCC 3540
Qy 3540 TCACCGTCAAGCTGCACCTGCTGAGCTGGGCGGAGCTGCGCCACTTCTGCAAGCC 3599
Db 3541 TCACCGTCAAGCTGCACCTGCTGAGCTGGGCGGAGCTGCGCCACTTCTGCAAGCC 3600
Qy 3600 TCAGAGCTGCTGGGAGCAATTTGGGCGGTATGGCAGCTCTGGGCTACCCACTGCCCC 3659
Db 3601 TCAGAGCTGCTGGGAGCAATTTGGGCGGTATGGCAGCTCTGGGCTACCCACTGCCCC 3660
Qy 3660 AGCCGCTGCTGGGAGTGAACCCACTTGGACTCTCTGGGCTGCGCCAGCTGCTCTCTCC 3719
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Qy 3720 AGAAGATGACAGCTTCTGGCTGCTGAGGAGCTGAGACCTGGCTGCTGGGCTGCGGCA 3779
Db 3721 AGAAGATGACAGCTTCTGGCTGCTGAGGAGCTGAGACCTGGCTGCTGGGCTGCGGCA 3780
Qy 3780 AGAAGTTCACCGGCTCAAGAGAGAGTGAAGCTTCCAGAGCTGAGTCAACCTGCAAC 3839
Db 3781 AGAAGTTCACCGGCTCAAGAGAGAGTGAAGCTTCCAGAGCTGAGTCAACCTGCAAC 3840
Qy 3840 TGGGGCTCATGGCTTCTGACTTCTGACCTTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3899
Db 3841 TGGGGCTCATGGCTTCTGACTTCTGACCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3900
Qy 3900 TCCCACTTTTGAGAGCCAGCCCTGTATGCCAAACCTGTTGAGCCAGGAGCAGAGCT 3959
Db 3901 TCCCACTTTTGAGAGCCAGCCCTGTATGCCAAACCTGTTGAGCCAGGAGCAGAGCT 3960

Qy 3960 GTGAGCCTTGGCCCTTTCTTGACCCGGCTGGGCGTGTGATGGATCAGGCCCTGTCTCTCT 4019
Db 3961 GTGAGCCTTGGCCCTTTCTTGACCCGGCTGGGCGTGTGATGGATCAGGCCCTGTCTCTCTCT 4020
Qy 4020 CCCACCTCTCCAAAGGCTCTACCGAGCTGGGAGGAGGTACAGTAGGCCCTGTCTCTCTCT 4079
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Qy 4260 TTTGGCTGCCCCACTCTCTCTTGGATGGGTTGCTCTCTTATCCCAATCACTCTATAC 4319
Db 4261 TTTGGCTGCCCCACTCTCTCTTGGATGGGTTGCTCTCTTATCCCAATCACTCTATAC 4320
Qy 4320 ATCCAAATTCAGGAACAAACATGCTGGCAATCTTACACAAAGAGATGAGATTACAGT 4379
Db 4321 ATCCAAATTCAGGAACAAACATGCTGGCAATCTTACACAAAGAGATGAGATTACAGT 4380
Qy 4380 GCAGGTTGGGCTCTGCTTGGAGTGGCTTATAAACAGAGAGAAATACTTGAAGCA 4439
Db 4381 GCAGGTTGGGCTCTGCTTGGAGTGGCTTATAAACAGAGAGAAATACTTGAAGCA 4440
Qy 4440 CAGGGCAGGAGCAGACAGACAGAGCCAGGAGTCTCCAAAGCAGAGTGGCAACAA 4499
Db 4441 CAGGGCAGGAGCAGACAGACAGAGCCAGGAGTCTCCAAAGCAGAGTGGCAACAA 4500
Qy 4500 AACCCGAGCTGAGCATCAGGACCTTGGCTCGAATTTCTTCCAGTATTACGGTGCCTCTT 4559
Db 4501 AACCCGAGCTGAGCATCAGGACCTTGGCTCGAATTTCTTCCAGTATTACGGTGCCTCTT 4560
Qy 4560 CTCTGCCCCCTTCCAGAGGTATCTGTGGGTTCCAGGCTGGGAGGAGCAACCATAGCCA 4619
Db 4561 CTCTGCCCCCTTCCAGAGGTATCTGTGGGTTCCAGGCTGGGAGGAGCAACCATAGCCA 4620
Qy 4620 CACCACAGGATTTCTGAAAGTTTACAAATGCACTAGCATTTTGGGTTGAGGTTGGCAGC 4679
Db 4621 CACCACAGGATTTCTGAAAGTTTACAAATGCACTAGCATTTTGGGTTGAGGTTGGCAGC 4680
Qy 4680 TCCCCAAGCCCTGCCCCCAGCCCAACCATCTGACTCTAAGTGTGTGTATTAAATA 4739
Db 4681 TCCCCAAGCCCTGCCCCCAGCCCAACCATCTGACTCTAAGTGTGTGTATTAAATA 4740
Qy 4740 TTTATTATTGGAGATGTTATTATTATTAGATGATATTATTGAGATTTCTATTCTTGT 4799
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Qy 4800 ATTAACAAATAAATGTTTGGCCCCAGAACTTAGTCTCTTGGCCCCAGCCTCACCCCTCTG 4859
Db 4801 ATTAACAAATAAATGTTTGGCCCCAGAACTTAGTCTCTTGGCCCCAGCCTCACCCCTCTG 4860
Qy 4860 GTGCTCATCAGACTCTTGCCACCCCTGGCTCCCACTCTCCCTGCTGCTCTGTTGGAGCTG 4919
Db 4861 GTGCTCATCAGACTCTTGCCACCCCTGGCTCCCACTCTCCCTGCTGCTCTGTTGGAGCTG 4920
Qy 4920 CACAGACTCTGGGAGAGGCGCTCTTCTCCCGCAGCTGGGGCGATGGGCGCACCTCAG 4979
Db 4921 CACAGACTCTGGGAGAGGCGCTCTTCTCCCGCAGCTGGGGCGATGGGCGCACCTCAG 4980
Qy 4980 ACTTACCCACTGCTGTCACCAACCAACCCCTTGTATCCCTGCTCTCTGCTCTCCACAGCTT 5039
Db 4981 ACTTACCCACTGCTGTCACCAACCAACCCCTTGTATCCCTGCTCTCTGCTCTCCACAGCTT 5040

QY 5040 CTGTCCACCCAGGTTTCCTCACCACCTTTGCTAAGTCTTCTCTCA 5087
 Db |||||
 5041 CTGTCCACCCAGGTTTCCTCACCACCTTTGCTAAGTCTTCTCTCA 5088
 |||||

RESULT 5
 AAA88546
 ID AAA88546 standard; DNA; 1790 BP.
 XX
 AC AAA88546;
 XX
 DT 22-JAN-2001 (first entry)
 XX
 DE Human interleukin-B60 (IL-B60) gene.
 XX
 KW Interleukin-B60; IL-B60; human; cytokine; chromosome 11;
 KW cytokine-like factor-1; haematopoietic; inflammation; antiinflammatory;
 KW autoimmune disease; therapy; ds.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH 162..809
 CDS /*tag= a
 FT sig_peptide 162..212
 FT /*tag= b
 FT mat_peptide 213..806
 FT /*tag= c

XX WO200053631-A1.
 XX
 XX 14-SEP-2000.
 PD
 XX 09-MAR-2000; 2000WO-US006182.
 XX
 XX 11-MAR-1999; 99US-00267901.
 XX
 XX (SCHE) SCHERING CORP.
 XX
 XX Oppmann B, Timans JC, Kastelein RA, Bazan JF;
 PI WPI; 2000-587426/55.
 DR P-PSDB; AAB19686.
 XX
 XX Cytokine-like factor 1 (CLF-1) and interleukin (IL)-B60 complexes,
 PT polypeptides, and nucleic acids, useful in research, diagnosis and for
 PT treating inflammatory and autoimmune disorders.
 XX
 PS Claim 17; Page 15-16; 97pp; English.
 XX
 CC The present sequence is that of DNA encoding human interleukin-B60 (IL-
 CC B60, see AAB19586), a novel, small soluble cytokine-like protein of 198
 CC amino acids that exhibits structural motifs characteristic of a member of
 CC the long-chain cytokines, and which shows homology to granulocyte colony
 CC stimulating factor and interleukin-6. IL-608 may have either stimulatory
 CC or inhibitory effects on haematopoietic cells, including e.g. lymphoid
 CC cells, such as T-cells, B-cells, natural killer cells, macrophages,
 CC dendritic cells, haematopoietic progenitors, etc. Methods are provided
 CC for modulating the physiology or development of a cell or tissue culture
 CC cells by contacting the cell with an agonist or antagonist of IL-B60 or
 CC an agonist of antagonist of a complex of mature IL-B60 and its partner,
 CC cytokine-like factor-1 (CLF-1, see AAB19588). The IL-B60/CLF-1 cytokine
 CC serves as a key physiological factor in motor neuron development and
 CC regeneration. IL-60B, its agonists and antagonists may be used to treat
 CC inflammatory or autoimmune disorders and also for drug screening. The
 CC IL60B gene maps to human chromosome 11
 XX
 XX Sequence 1790 BP; 381 A; 560 C; 474 G; 375 T; 0 U; 0 Other;
 SQ

Query Match 28.8%; Score 1464.4; DB 3; Length 1790;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1465; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

3363 AGTGAATACCTGGGCCCCCTTTCAAGAGCCAGACTTCAACCTCCCCCTGGGG 3422
 313 ATCTGAACCTACCTGGGCCCCCTTTCAAGAGCCAGACTTCAACCTCCCCCTGGGG 372
 3423 CAGAGACTCTGCCAGGGCCACTGTGACTTGGAGGTGGGAGCTCAATGACAAAC 3482
 373 CAGAGACTCTGCCAGGGCCACTGTGACTTGGAGGTGGGAGCTCAATGACAAAC 432
 3483 TGGGCTGACCCAGAACTACAGAGGCTACAGCCACTTCTGTGTACTTGGCTGCTCA 3542
 433 TGGGCTGACCCAGAACTACAGAGGCTACAGCCACTTCTGTGTACTTGGCTGCTCA 492
 3543 ACCGTGAGGCTGCTGCTGAGCTGGGCGGAGGCTGGCCACTTCTGACACAGCTCC 3602
 493 ACCGTGAGGCTGCTGCTGAGCTGGGCGGAGGCTGGCCACTTCTGACACAGCTCC 552
 3603 AGGGCTGCTGGGAGCATTTGGGGCGTCAATGGAGCTCTGGGCTACCCACTGCCCCAGC 3662
 553 AGGGCTGCTGGGAGCATTTGGGGCGTCAATGGAGCTCTGGGCTACCCACTGCCCCAGC 612
 3663 CGTCTGGGACTGAACCCACTTGGACTCTGGGCTGCCCCAGAGTGAATTCCTCCAGA 3722
 613 CGTCTGGGACTGAACCCACTTGGACTCTGGGCTGCCCCAGAGTGAATTCCTCCAGA 672
 3723 AGATGAGACACTTCTGGCTGCTGAAGGAGCTGCAGACCTGGGCTGGGCGCTCGGCCAAG 3782
 673 AGATGAGACACTTCTGGCTGCTGAAGGAGCTGCAGACCTGGGCTGGGCGCTCGGCCAAG 732
 3783 ACTTCAACCGGCTCAAGAAAGATGCAGCTCCAGAGCTGCAGTCACTCCCTGCACCTGG 3842
 733 ACTTCAACCGGCTCAAGAAAGATGCAGCTCCAGAGCTGCAGTCACTCCCTGCACCTGG 792
 3843 GGGCTCATGGCTTCTGACTTCTGACTTCTCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 3902
 793 GGGCTCATGGCTTCTGACTTCTGACTTCTCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 852
 3903 CACTTTGTGAGAGCCAGCCCTGTATGCCAAACCTGTTTTCAGCCAGGAGACAGAGCTGTG 3962
 853 CACTTTGTGAGAGCCAGCCCTGTATGCCAAACCTGTTTTCAGCCAGGAGACAGAGCTGTG 912
 3963 AGCTCTGGCCCTTCTGAGACCGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCT 4022
 913 AGCTCTGGCCCTTCTGAGACCGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCT 972
 4023 CACTTCCCAAGAGTCTACCGAGCTGGGAGGAGGTACAGTAGGCTGCTGCTGCTGCTGCTGCT 4082
 973 CACTTCCCAAGAGTCTACCGAGCTGGGAGGAGGTACAGTAGGCTGCTGCTGCTGCTGCTGCT 1032
 4083 TCTACAGGAAGTCTATGCTCGAGGAGTGTGAAGTGGTTTTCAGGTGGTGCAGAGGCTCA 4142
 1033 TCTACAGGAAGTCTATGCTCGAGGAGTGTGAAGTGGTTTTCAGGTGGTGCAGAGGCTCA 1092
 4143 TGGCTCTCTGCTTCTTGGCTTACACTTGGCCAGTGGCCAGCCAGCCCTCAGTGGCACA 4202
 1093 TGGCTCTCTGCTTCTTGGCTTACACTTGGCCAGTGGCCAGCCAGCCCTCAGTGGCACA 1152
 4203 TCTGAGGAGCGGGGTGAGGGGCGCCACACCATGCTTCTTGGGCTGAAGCCCTT 4262
 1153 TCTGAGGAGCGGGGTGAGGGGCGCCACACCATGCTTCTTGGGCTGAAGCCCTT 1212
 4263 GGTGCTGCCACTCTCTCTGGATGGGTGTGCTTCTTCTTATCCCAATCACTCTATACATC 4322
 1213 GGTGCTGCCACTCTCTCTGGATGGGTGTGCTTCTTCTTATCCCAATCACTCTATACATC 1272
 4323 CAATTGAGGAACAACAATGTTGGCAATTTCTACAAAAGAGATGAGATTAAACAGTGA 4382
 1273 CAATTGAGGAACAACAATGTTGGCAATTTCTACAAAAGAGATGAGATTAAACAGTGA 1332
 4383 GGGTTGGGTTCTCAATTGGAGGTGCTTATAAACAGAGAGAAAATATCTGAAAGCACAG 4442
 1333 GGGTTGGGTTCTCAATTGGAGGTGCTTATAAACAGAGAGAAAATATCTGAAAGCACAG 1392
 4443 GGGCAGGACAGACAGACAGACCCAGGAGTCTCCAAAGACAGAGTGGCAACAAAC 4502

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Db      1393 GGCAGGGAGAGACAGACAGACAGAGAGTCTCCAAAGCAGAGTGCAGAAAC 1452
Qy      4503 CCAGAGCTGAGCATCAGAGACCTTGCCTCGAATTGTCTTCCAGTATTACGGTGCCTTCTTC 4562
Db      1453 CCAGAGCTGAGCATCAGAGACCTTGCCTCGAATTGTCTTCCAGTATTACGGTGCCTTCTTC 1512
Qy      4563 TGCCCTCTTCCAGAGGTATCTGTGGTTGCCAGGTGCGGAGGGGCAACCATAGCACAC 4622
Db      1513 TGCCCTCTTCCAGAGGTATCTGTGGTTGCCAGGTGCGGAGGGGCAACCATAGCACAC 1572
Qy      4623 CACAGGATTTCTGAAAGTTTCAATGCGAGTAGCATTTTGGGTGTAGGCTGCCAGCTCC 4682
Db      1573 CACAGATTTCTGAAAGTTTCAATGCGAGTAGCATTTTGGGTGTAGGCTGCCAGCTCC 1632
Qy      4683 CCAAGGCTGCGCCCGCAGCCCGCAGCTCATGACTCTAAGTGTGTTTATTAATATT 4742
Db      1633 CCAAGGCTGCGCCCGCAGCCCGCAGCTCATGACTCTAAGTGTGTTTATTAATATT 1692
Qy      4743 ATTTATTTGAGATGTTATTTATTTAGATGATATTATTCAGAAATTTCTATTCTTGTATT 4802
Db      1693 ATTTATTTGAGATGTTATTTATTTAGATGATATTATTCAGAAATTTCTATTCTTGTATT 1752
Qy      4803 AACAAATAAAATGCTTGCCCGCAGAAC 4828
Db      1753 AACAAATAAAATGCTTGCCCGCAGAAC 1778

RESULT 6
AXX16161
ID AAX16161 standard; DNA; 1710 BP.
AC AAX16161;
XX
XX
DT 28-APR-1999 (first entry)
XX
DE Human cardiotrophin-like cytokine encoding DNA.
XX
KW Human; cardiotrophin-like cytokine; interleukin 6 cytokine family; CLC;
KW IL-6; diagnosis; detection; immune system-related disorder; cancer;
KW cardiac disorder; heart failure; hypertension; cancer;
KW autoimmune disorder; infection; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 46..723
FT /tag= a
FT sig_peptide 46..129
FT /tag= b
FT mat_peptide 130..720
FT /tag= c
FT /product= "cardiotrophin-like cytokine"
FT
XX
PN WO9900415-A1.
XX
XX 07-JAN-1999.
XX
XX 29-JUN-1998; 98WO-US013129.
XX
XX 30-JUN-1997; 97US-0051311P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
PI Shi Y, Ruben SM;
XX
XX WPI; 1999-095678/08.
XX
XX P-PSDB; AAW94466.
XX
XX New isolated cardiotrophin-like cytokine nucleic acid - used to develop
XX products for treating cardiac and immune system disorders, e.g. heart
XX failure, hypertension, cancers, autoimmune disorders and infections.
XX

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PS Claim 2; Fig 1; 103pp; English.
XX
CC The present invention relates to a novel cardiotrophin-like cytokine
CC (CLC) protein which is a member of the interleukin 6 (IL-6) cytokine
CC family. The present sequence encodes the human CLC protein. The present
CC invention also describes screening methods for identifying agonists and
CC antagonists of CLC activity, as well as methods for detecting cardiac and
CC immune system-related disorders and therapeutic methods for treating
CC cardiac and immune system-related disorders, e.g. heart failure,
CC hypertension, cancers, autoimmune disorders and infections.
XX
SQ Sequence 1710 BP; 370 A; 530 C; 448 G; 362 T; 0 U; 0 Other;

Query Match      28.88; Score 1463.4; DB 2; Length 1710;
Best Local Similarity 99.99; Pred. No. 0;
Matches 1464; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      3363 AGCTGAACCTACCTGGGCCCCCTTTCAACGAGCCAGACTTTCAACCTCCCGCTGGGG 3422
Db      227 ATCTGAACCTACCTGGGCCCCCTTTCAACGAGCCAGACTTTCAACCTCCCGCTGGGG 286
Qy      3423 CAGAGACTCTGCCAGGCGCCACTGTTGACTTGAGGTGGCGAAGCTCAATGACAAAC 3482
Db      287 CAGAGACTCTGCCAGGCGCCACTGTTGACTTGAGGTGGCGAAGCTCAATGACAAAC 346
Qy      3483 TCGGCTGAGCCAGAACTACGAGGCTTACAGCCACTTCTGTGTTACTTTCGTGGGCTCA 3542
Db      347 TCGGCTGAGCCAGAACTACGAGGCTTACAGCCACTTCTGTGTTACTTTCGTGGGCTCA 406
Qy      3543 ACCGTAGGCTGCCACTGCTGAGTGGCGGAGCTTGGCCCACTTCTGACCCAGGCTCC 3602
Db      407 ACCGTAGGCTGCCACTGCTGAGTGGCGGAGCTTGGCCCACTTCTGACCCAGGCTCC 466
Qy      3603 AGGCGCTGCTGGGCGAGCATTTGGCGGTCTATGCGAGCTTGGGCTACCCACTGCCCGAGC 3662
Db      467 AGGCGCTGCTGGGCGAGCATTTGGCGGTCTATGCGAGCTTGGGCTACCCACTGCCCGAGC 526
Qy      3663 CGTGTCTGGGACTGAACCCACTTGGACTCTCTGGCTGCCACAGTACTTCTCTCAGA 3722
Db      527 CGTGTCTGGGACTGAACCCACTTGGACTCTCTGGCTGCCACAGTACTTCTCTCAGA 586
Qy      3723 AGATGAGAGCTTCTGCTGCTGAGAGAGCTGAGACCTTGGCTGGCGCTGGCCCAAG 3782
Db      587 AGATGAGAGCTTCTGCTGCTGAGAGAGCTGAGACCTTGGCTGGCGCTGGCCCAAG 646
Qy      3783 ACTTCAACCGGCTCAAGAAGAAGATGAGCTCCAGAGCTGAGTCACTCCCTGCACCTGG 3842
Db      647 ACTTCAACCGGCTCAAGAAGAAGATGAGCTCCAGAGCTGAGTCACTCCCTGCACCTGG 706
Qy      3843 GGGCTCATGGCTTCTGACTTCTGACTTCTCTCTGCTTCCCTCCCTTCAACCTCTCTCC 3902
Db      707 GGGCTCATGGCTTCTGACTTCTGACTTCTCTCTGCTTCCCTTCAACCTCTCTCC 766
Qy      3903 CACTTCTGAGAGCCAGCCCTGTATGCCAACACTTGTAGCCAGGAGAGACAGAGTGTG 3962
Db      767 CACTTCTGAGAGCCAGCCCTGTATGCCAACACTTGTAGCCAGGAGAGACAGAGTGTG 826
Qy      3963 AGCCTCTGGCCCTTCTCTGAGCCGGCTGGCGGTGATGCGATCAGCCCTGTCTCTCC 4022
Db      827 AGCCTCTGGCCCTTCTCTGAGCCGGCTGGCGGTGATGCGATCAGCCCTGTCTCTCC 886
Qy      4023 CACCTCCCAAGGTCTACCGAGCTGGGAGAGGTACAGTGGCCCTGTCTCTCTGT 4082
Db      887 CACCTCCCAAGGTCTACCGAGCTGGGAGAGGTACAGTGGCCCTGTCTCTGT 946
Qy      4083 TCTACAGAGAGTCAATGCTCGAGGAGGTGAAGTGTTCAGGTTGTGAGAGGCGCTCA 4142
Db      947 TCTACAGAGAGTCAATGCTCGAGGAGGTGAAGTGTTCAGGTTGTGAGAGGCGCTCA 1006
Qy      4143 TGGCTCTCTCTCTTCTTACCTTACCTTGGCGAGTGGCCAGCCCTCAGGTGGCACA 4202
Db      1007 TGGCTCTCTCTCTTCTTACCTTACCTTGGCGAGTGGCCAGCCCTCAGGTGGCACA 1066

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RESULT 8
 AAD04201
 ID AAD04201 standard; cDNA; 729 BP.
 XX AC AAD04201;
 XX DT 02-JUL-2001 (first entry)
 XX DE Human cardiotrophin-like cytokine (CLC) cDNA.
 XX KW Human; biologically active complex; haemopoietin receptor; NR6;
 KW cardiotrophin-like cytokine; CLC; therapy; prophylaxis; proliferation;
 KW differentiation; cell survival; neurotrophic activity; ss.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 FT CDS 11..679
 FT FT /*tag= a
 FT FT /product= "Human cardiotrophin-like cytokine (CLC)
 FT FT protein"
 FT FT /note= "CDS does not include stop codon"
 FT FT /partial
 FT FT sig_peptide 11..91
 FT FT /*tag= b
 FT FT mat_peptide 92..679
 FT FT /*tag= c
 FT FT /product= "Human mature cardiotrophin-like cytokine (CLC)
 FT FT protein"
 XX WO200127157-A1.
 XX PN 19-APR-2001.
 XX PD 06-OCT-2000; 2000WO-AU001216.
 XX PF 08-OCT-1999; 99AU-00003327.
 XX PR 12-MAY-2000; 2000AU-00007489.
 XX PA (AMRA-) AMRAD OPERATIONS PTY LTD.
 XX PI Nash A, Jachno KM, Fabri LJ, Reid K, Bartlett PF, Hilton DJ;
 PI Nakata Y, Hasegawa M;
 XX WPI; 2001-281978/29.
 DR P-PSDB; AAE00828.
 XX New biologically active complex comprising NR6 and cardiotrophin-like-
 PT cytokine, for facilitating proliferation, differentiation and/or survival
 PT of a cell.
 XX Claim 31; Page 112-114; 123pp; English.
 XX The present invention relates to a biologically active complex comprising
 CC a haemopoietin receptor, NR6 and cardiotrophin-like cytokine (CLC). The
 CC complex is useful in the manufacture of a medicament for the treatment
 CC and/or prophylaxis of a subject, as it is involved in facilitating
 CC proliferation, differentiation and/or survival of a cell. The complex or
 CC its components have neurotrophic activity. The present sequence is human
 CC cardiotrophin-like cytokine (CLC) cDNA
 XX SQ Sequence 729 BP; 132 A; 261 C; 196 G; 140 T; 0 U; 0 Other;
 Query Match 10.4%; Score 529.4; DB 4; Length 729;
 Best Local Similarity 99.8%; Pred. No. 8.9e-121;
 Matches 530; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 3363 AGCTGAACCTACCTGGGCCCCCTTTTCAAGAGCCAGACTTCAACCCCTCCGCGCTGGGG 3422
 192 ATCTGAACCTACCTGGGCCCCCTTTTCAAGAGCCAGACTTCAACCCCTCCGCGCTGGGG 251

QY 3423 CAGAGACTCTGCCAGGCGCCACTTTGACTTGGAGGTGTGGCGAAGCCTCAATGACAAAC 3482
 DB 252 CAGAGACTCTGCCAGGCGCCACTTTGACTTGGAGGTGTGGCGAAGCCTCAATGACAAAC 311
 QY 3483 TCGGGCTGAGCCAGAACTAGAGCCCTACAGCCACCTTCTGTGTACTTGGTGGGCTCA 3542
 DB 312 TCGGGCTGAGCCAGAACTAGAGCCCTACAGCCACCTTCTGTGTACTTGGTGGGCTCA 371
 QY 3543 ACCGTCAAGGCTGCCACTGTGAGCTGCGCGCGAGCCCTGGGCCACTTCTGCACAGCCCTCC 3602
 DB 372 ACCGTCAAGGCTGCCACTGTGAGCTGCGCGCGAGCCCTGGGCCACTTCTGCACAGCCCTCC 431
 QY 3603 AGGCGCTGTGGGAGCATTGCGGGCGCTATGGAGCTCTGGGCTACCCACTGCCCCAGC 3662
 DB 432 AGGCGCTGTGGGAGCATTGCGGGCGCTATGGAGCTCTGGGCTACCCACTGCCCCAGC 491
 QY 3663 CGCTGCCTGGGACTGAACCCACTTGGACTCTGGCCCTGCCACAGTGACTTCTCTCCAGA 3722
 DB 492 CGCTGCCTGGGACTGAACCCACTTGGACTCTGGCCCTGCCACAGTGACTTCTCTCCAGA 551
 QY 3723 AGATGAGACTTCTGGCTGCTGAAGAGCTGAGACCTGGCTGGCGCTCGCCCAAGG 3782
 DB 552 AGATGAGACTTCTGGCTGCTGAAGAGCTGAGACCTGGCTGGCGCTCGCCCAAGG 611
 QY 3783 ACTTCACCGGCTCAGAGAAGATGCAGCTCCAGCAGCTGCAGTCCACCTGCACCTGG 3842
 DB 612 ACTTCACCGGCTCAGAGAAGATGCAGCTCCAGCAGCTGCAGTCCACCTGCACCTGG 671
 QY 3843 GGGCTCATGCTTCTGACTTCTGACCTTCTCTCTTCTGGTCCCTCCCTTCAA 3893
 DB 672 GGGCTCATGCTTCTGACTTCTGACCTTCTCTCTTCTGGTCCCTCCCTTCAA 722

RESULT 9
 AAH74484
 ID AAH74484 standard; DNA; 881 BP.
 XX AC AAH74484;
 XX DT 15-OCT-2001 (first entry)
 XX DE Nucleotide sequence of a human NNT-1 protein.
 XX KW NNT-1; CLP-1; SCNTFRAlpha; nervous system; neuron; nervous system;
 KW neuro-muscular function; tumour; immune system; haematopoietic system;
 KW reproductive system; liver; skeletal muscle; neurodegenerative disease;
 KW amyotrophic lateral sclerosis; Parkinson's disease; Huntington's disease;
 KW muscular mass; paralysis; cancer; obesity; fertility; endometriosis;
 KW blastocyst implantation; thrombosis; retinal disease;
 KW retinal pigmentosis; ss.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 FT CDS 174..851
 FT FT /*tag= a
 FT FT /product= "NNT-1"
 XX WO200155172-A2.
 XX PD 02-AUG-2001.
 XX PF 26-JAN-2001; 2001WO-FR000253.
 XX PR 27-JAN-2000; 2000FR-00001035.
 XX PR 12-OCT-2000; 2000FR-00013089.
 XX PA (FABR) FABRE MEDICAMENT SA PIERRE.
 XX PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 XX PI Elson G, Gauchat J, Plun-Favreau H, Chevalier S, Gascan H;
 XX WPI; 2001-488773/53.

DR P-PSDB; AAG63543.
XX
PT A complex comprising a NNT-1 protein and a Clf-1 and/or SCNTFRalpha
PT protein useful to treat neurodegenerative disease including Parkinson's
PT and Huntington's, obesity and cancer.
XX
PS Disclosure; Page 57-58; 67pp; French.
XX
CC The present sequence encodes a human NNT-1 protein. The specification
CC describes a complex comprising a NNT-1 protein and a Clf-1 and/or
CC SCNTFRalpha protein. The NNT-1/Clf-1 complex is used to modulate activity
CC of the SCNTFRalpha/gp130/LIFRbeta receptor complex, or to induce
CC phosphorylation of the tyrosine of gp130 and LIFRbeta, particularly where
CC cells expressing the receptor complex are in the central or peripheral
CC nervous system, in neurons implicated in neuro-muscular function or in
CC skeletal muscle. The complex or antibodies are also used to decrease the
CC survival, growth or proliferation of tumour cells or to facilitate the
CC proliferation and/or inhibit differentiation of cells stocks. The complex
CC is also used to modulate activity of the gp130/LIFRbeta receptor or cells
CC expressing that receptor, particularly those cells implicated in the
CC immune, haematopoietic, nervous or reproductive system, the liver or
CC skeletal muscle. Molecules of the invention may be used to prevent or
CC treat neurodegenerative diseases including amyotrophic lateral sclerosis,
CC Parkinson's and Huntington's disease, to repair or regenerate nervous or
CC muscular tissue or to maintain muscular mass in paralysis patients. They
CC may also be used to treat cancer, obesity and associated diseases, and to
CC improve fertility, particularly to avoid endometriosis and/or assist
CC blastocyst implantation, thrombosis, or retinal disease, particular
CC retinal pigmentosis
XX
SQ Sequence 881 BP; 158 A; 318 C; 246 G; 159 T; 0 U; 0 Other;
Query Match 10.3%; Score 525.4; DB 4; Length 881;
Best Local Similarity 99.8%; Pred. No. 9.6e-120;
Matches 526; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3363 AGCTGAACCTACTGGGCCCCCTTCAACGAGCAGACTTCAACCTCCCGCTGGGG 3422
DB 355 ATCTGAACCTACTGGGCCCCCTTCAACGAGCAGACTTCAACCTCCCGCTGGGG 414
QY 3423 CAGAGACTCTGCCAGGCGCACTGTGACTTGGAGGTGTGGAGGCTCAATGACAAAC 3482
DB 415 CAGAGACTCTGCCAGGCGCACTGTGACTTGGAGGTGTGGAGGCTCAATGACAAAC 474
QY 3483 TCGGCTGACCCAGAACTACGAGGCTTACGCCACCTTCTGTACTTGGCTGCTCA 3542
DB 475 TCGGCTGACCCAGAACTACGAGGCTTACGCCACCTTCTGTACTTGGCTGCTCA 534
QY 3543 ACCGTCAGGCTGCCACTCTGAGCTGCGCGCAGCTGGCCACTTCTGACACGAGCTCC 3602
DB 535 ACCGTCAGGCTGCCACTCTGAGCTGCGCGCAGCTGGCCACTTCTGACACGAGCTCC 594
QY 3603 AGGGCTCTGGCAGCACTTGGGCGTCACTGGCAGCTCTGGGCTACCCACTGCCCGAGC 3662
DB 595 AGGGCTCTGGCAGCACTTGGGCGTCACTGGCAGCTCTGGGCTACCCACTGCCCGAGC 654
QY 3663 CGCTGCTGGAGTGAACCCACTTGGACTCTGGCCCTGCCCACAGTGAATCTCTCAGA 3722
DB 655 CGCTGCTGGAGTGAACCCACTTGGACTCTGGCCCTGCCCACAGTGAATCTCTCAGA 714
QY 3723 AGATGAGAGACTTCTGGCTGTGAAGGAGCTGCAGACCTGGCTGTGGGCTCGGCCAAGG 3782
DB 715 AGATGAGAGACTTCTGGCTGTGAAGGAGCTGCAGACCTGGCTGTGGGCTCGGCCAAGG 774
QY 3783 ACTTCAACCGGCTCAAGAAGAAGATGACAGCTTCCAGAGCTGCACTACCTGACCTGG 3842
DB 775 ACTTCAACCGGCTCAAGAAGAAGATGACAGCTTCCAGAGCTGCACTACCTGACCTGG 834
QY 3843 GGGCTCATGGCTTCTGACTTCTGACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3889
DB 835 GGGCTCATGGCTTCTGACTTCTGACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 881

RESULT 10
AAV22652
ID AAV22652 standard; cDNA; 797 BP.
XX
AC AAV22652;
XX
DT 13-JUL-1998 (first entry)
XX
DE cDNA encoding human neurotrophic factor NNT-1.
XX
KW Human; neurotrophic factor; NNT-1; growth; motor; sympathetic; neuron;
KW treatment; neurological disease; degeneration; Parkinson's disease;
KW amyotrophic lateral sclerosis; ALS; Alzheimer's disease; stroke; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
CDS 90..767
FT sig_peptide /tag= a
FT 90..170
FT mat_peptide /tag= b
FT 171..764
FT /tag= c
XX
US5741772-A.
XX
PN 21-APR-1998.
XX
PD 03-FEB-1997; 97US-00792019.
XX
PR 03-FEB-1997; 97US-00792019.
XX
PA (AMGE-) AMGEN INC.
XX
PI Chang M;
XX
DR WPI; 1998-260526/23.
DR P-PSDB; AAM56141.
XX
PT Neurotrophic factor NNT-1 polypeptide and related nucleic acids - useful
PT for stimulating growth of motor and sympathetic neurons.
XX
PS Disclosure; Fig 1; 41pp; English.
XX
CC The present sequence encodes a human neurotrophic factor, designated NNT-
CC 1, which is capable of stimulating growth of motor or sympathetic
CC neurons. The NNT-1 protein is useful in the treatment of neurological
CC diseases characterised by the degeneration and death of particular
CC classes of neurons. These diseases specifically include Parkinson's
CC disease, amyotrophic lateral sclerosis (ALS), Alzheimer's disease, stroke
CC and various degenerative disorders affecting vision
XX
SQ Sequence 797 BP; 139 A; 297 C; 218 G; 143 T; 0 U; 0 Other;
Query Match 10.3%; Score 523.4; DB 2; Length 797;
Best Local Similarity 99.8%; Pred. No. 2.9e-119;
Matches 524; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3363 AGCTGAACCTACTGGGCCCCCTTCAACGAGCAGACTTCAACCTCCCGCTGGGG 3422
DB 271 ATCTGAACCTACTGGGCCCCCTTCAACGAGCAGACTTCAACCTCCCGCTGGGG 330
QY 3423 CAGAGACTCTGCCAGGCGCACTGTGACTTGGAGGTGTGGAGGCTCAATGACAAAC 3482
DB 331 CAGAGACTCTGCCAGGCGCACTGTGACTTGGAGGTGTGGAGGCTCAATGACAAAC 390
QY 3483 TCGGCTGACCCAGAACTACGAGGCTTACAGCCACCTTCTGTGTTACTTGGCTGCTCA 3542
DB 391 TCGGCTGACCCAGAACTACGAGGCTTACAGCCACCTTCTGTGTTACTTGGCTGCTCA 450
QY 3543 ACCGTCAGGCTGCCACTCTGAGCTGCGCGCAGCTGGCCACTTCTGTCACACGAGCTCC 3602
DB 451 ACCGTCAGGCTGCCACTCTGAGCTGCGCGCAGCTGGCCACTTCTGTCACACGAGCTCC 510

QY 3603 AGGCGCTGCTGGCAGCATTGGCGGCGTCAATGSCAGCTCTGGGCTACCCACCTGCCCGCAGC 3662
 DB |||||
 QY 511 AGGCGCTGCTGGCAGCATTGGCGGCGTCAATGSCAGCTCTGGGCTACCCACCTGCCCGCAGC 570
 DB |||||
 QY 3663 CGCTGCTGGGACTGAACCCACTTGGACTCTGGCCCTGCCACAGTGACTTCTCTCCAGA 3722
 DB |||||
 QY 571 CGCTGCTGGGACTGAACCCACTTGGACTCTGGCCCTGCCACAGTGACTTCTCTCCAGA 630
 DB |||||
 QY 3723 AGATGACGACTTCTGGCTGCTGAAGAGCTGCAGACCTGGTGTGGCGCTGGCCAGG 3782
 DB |||||
 QY 631 AGATGACGACTTCTGGCTGCTGAAGAGCTGCAGACCTGGTGTGGCGCTGGCCAGG 690
 DB |||||
 QY 3783 ACTTCAACCGGCTCAAGAGAAGATGCAGCTCCAGCAGCTGCAGTCAACCTGCCCTGG 3842
 DB |||||
 QY 691 ACTTCAACCGGCTCAAGAGAAGATGCAGCTCCAGCAGCTGCAGTCAACCTGCCCTGG 750
 DB |||||
 QY 3843 GGGCTCATGGCTTCTGACTTCTGACCTTCTCCTTCTGGCTCCGCC 3887
 DB |||||
 QY 751 GGGCTCATGGCTTCTGACTTCTGACCTTCTCCTTCTGGCTCCGCC 795

RESULT 11

AAV47510
 ID AAV47510 standard; cDNA; 797 BP.

XX AC AAV47510;
 AC

DT 09-NOV-1998 (first entry)
 DT

XX Human neurotrophic factor NNT-1 cDNA.
 DE

XX NNT-1; neurotrophic factor; human; antiinflammatory; adjuvant;
 KW Alzheimer's disease; Parkinson's disease; Huntington's disease;
 KW amyotrophic lateral sclerosis; Charcot-Marie-Tooth syndrome;
 KW peripheral neuropathy; dystrophy; neural retina degeneration;
 KW common variable immunodeficiency; CVID; selective IgA deficiency;
 KW hypogammaglobulinaemia; X-linked agammaglobulinaemia; antiseptic;
 KW therapy; ss.

XX Homo sapiens.
 OS

XX Key Location/Qualifiers
 PH CDS 90..767
 FT /*tag= a

FT sig_peptide 90..170
 FT /*tag= b

FT mat_peptide 171..764
 FT /*tag= c

XX WO9833922-A1.
 PN

XX 06-AUG-1998.
 PD

XX 02-FEB-1998; 98WO-US002363.
 XX PF

XX 03-FEB-1997; 97US-00792019.
 PR

XX 30-JAN-1998; 98US-00016534.
 PR

XX (AMGE-) AMGEN INC.
 PA

XX Chang M, Elliot GS, Senaldi G, Sarmiento U;
 PI

XX WPI; 1998-437475/37.
 DR

XX P-PSDB; AAW29715.
 DR

XX Newly isolated nucleic acid encoding human or murine neurotrophic factor
 PT NNT-1 - useful for treatment of neurological and immunological diseases
 PT or inflammation, also as vaccine adjuvant.

XX Claim 3; Fig 1; 120pp; English.
 PS

XX This newly isolated human cDNA sequence (deposited at ATCC 98295) codes
 CC

CC for a novel neurotrophic factor, designated NNT-1 (see AAW29715), that is
 CC a growth factor for neurons and for B or T cells. It was obtained from a
 CC T-cell lymphoma cDNA library by expressed sequence tag analysis on the
 CC basis of homology to CNTF. The isolated NNT-1 cDNA was used as probe to
 CC isolated NNT-1 genomic DNA (see AAW47511). Vectors containing the cDNA or
 CC genomic DNA and host cells are provided for use in the production of NNT-
 CC 1 polypeptides. These are used to treat: (i) neurological or
 CC immunological diseases, specifically Alzheimer's, Parkinson's or
 CC Huntington's diseases, amyotrophic lateral sclerosis, Charcot-Marie-Tooth
 CC syndrome, peripheral neuropathy, dystrophy and degeneration of the neural
 CC retina, or conditions characterised by T or B cell defects, e.g. common
 CC variable immunodeficiency (CVID), selective IgA deficiency,
 CC hypogammaglobulinaemia and X-linked agammaglobulinaemia (claimed), but
 CC many others disclosed; and (ii) inflammation. NNT-1 is also able to boost
 CC immunoreactivity and antibody production following vaccination, and,
 CC since it inhibits tumour necrosis factor production, it may also be
 CC useful for treating sepsis. NNT-1 nucleic acid fragments are also used as
 CC hybridisation probes in diagnostic assays. In addition, cells that have
 CC been engineered to express NNT-1 can be implanted, or nucleic acids are
 CC delivered in gene therapy vectors

XX Sequence 797 BP; 139 A; 297 C; 218 G; 143 T; 0 U; 0 Other;

Query Match 10.38; Score 523.4; DB 2; Length 797;

Best Local Similarity 99.8%; Pred. No. 2.9e-119;

Matches 524; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3363 AGCTGAATACCTGGGCCCCCTTTCAACGAGCCAGACTTCAACCTCCCGCTGGGG 3422

DB 271 ATCTGAATACCTGGGCCCCCTTTCAACGAGCCAGACTTCAACCTCCCGCTGGGG 330

QY 3423 CAGAGACTTGCACAGGCGCACTGTGACTTGAGGTGCGAAGCTCAATGACAAC 3482

DB 331 CAGAGACTTGCACAGGCGCACTGTGACTTGAGGTGCGAAGCTCAATGACAAC 330

QY 3483 TCGCGCTGACCCAGAACTACGAGCGCTTACAGCCACCTCTGTGTACTTCGCTGGCTCA 3542

DB 391 TCGCGCTGACCCAGAACTACGAGCGCTTACAGCCACCTCTGTGTACTTCGCTGGCTCA 450

QY 3543 ACCGTAGGCTGCCACCTGTGAGTGGCGCGAGCGCTGGCCCACTTGTGACACAGCTCC 3602

DB 451 ACCGTAGGCTGCCACCTGTGAGTGGCGCGAGCGCTGGCCCACTTGTGACACAGCTCC 510

QY 3603 AGGCGCTGCTGGCAGCATTGGCGGCGTCAATGSCAGCTCTGGGCTACCCACCTGCCCGCAGC 3662

DB 511 AGGCGCTGCTGGCAGCATTGGCGGCGTCAATGSCAGCTCTGGGCTACCCACCTGCCCGCAGC 570

QY 3663 CGCTGCTGGGACTGAACCCACTTGGACTCTGGCCCTGCCACAGTGACTTCTCTCCAGA 3722

DB 571 CGCTGCTGGGACTGAACCCACTTGGACTCTGGCCCTGCCACAGTGACTTCTCTCCAGA 630

QY 3723 AGATGACGACTTCTGGCTGCTGAAGAGCTGCAGACCTGGTGTGGCGCTGGCCAGG 3782

DB 631 AGATGACGACTTCTGGCTGCTGAAGAGCTGCAGACCTGGTGTGGCGCTGGCCAGG 690

QY 3783 ACTTCAACCGGCTCAAGAGAAGATGCAGCTCCAGCAGCTGCAGTCAACCTGCCCTGG 3842

DB 691 ACTTCAACCGGCTCAAGAGAAGATGCAGCTCCAGCAGCTGCAGTCAACCTGCCCTGG 750

QY 3843 GGGCTCATGGCTTCTGACTTCTGACCTTCTCCTTCTGGCTCCGCC 3887

DB 751 GGGCTCATGGCTTCTGACTTCTGACCTTCTCCTTCTGGCTCCGCC 795

RESULT 12

AAA39481

ID AAA39481 standard; cDNA; 797 BP.

XX AC AAA39481;

XX AC AAA39481;

XX 24-AUG-2000 (first entry)

XX Human NNT-1 cDNA.

XX NNT-1; human; neurotrophic factor; neurotrophic; neuroprotective; treatment;
 KW anticonvulsant; aniparkinsonian; antidiabetic; ophthalmological;
 KW nervous system degeneration; Alzheimer's disease; Parkinson's disease;
 KW amyotrophic lateral sclerosis; Charcot-Marie-Tooth syndrome;
 KW Huntington's disease; peripheral neuropathy; neural retina degeneration;
 KW retinopathy; immune disorder; hematopoietic disorder; ss.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 FH CDS 90..767
 FT /*tag= a
 FT /product= "NNT-1"
 XX US6054294-A.
 XX 25-APR-2000.
 XX 12-DEC-1997; 97US-00988819.
 XX 03-FEB-1997; 97US-00792019.
 XX (AMGE-) AMGEN INC.
 XX Chang M;
 XX WPI; 2000-338492/29.
 XX P-PSDB; RAY87813.
 XX New nucleic acids encoding neurotrophic factors useful for stimulating
 FT growth of motor or sympathetic neurons for treating neuron cell damage.
 XX Claim 1a; Fig 1; 42pp; English.
 XX This invention describes a novel nucleic acid molecule (I) encoding a
 CC novel neurotrophic factor (NNT-1) (II) which has neurotrophic
 CC neuroprotective, anticonvulsant, antiparkinsonian, antidiabetic and
 CC ophthalmological activity. (I) is useful for producing NNT-1 polypeptides
 CC which are useful for treating patients in whom various cells of the
 CC central, autonomic, or peripheral nervous system have degenerated and/or
 CC have been damaged by congenital disease, trauma, mechanical damage,
 CC surgery, stroke, ischemia, infection, metabolic disease, nutritional
 CC deficiency, malignancy and/or toxic agents. NNT-1 proteins are used to
 CC treat diseases like Alzheimer's, Parkinson's, amyotrophic lateral
 CC sclerosis, Charcot-Marie-Tooth syndrome, Huntington's disease, peripheral
 CC neuropathy induced by diabetes or other metabolic disorders, and/or
 CC dystrophies or degeneration of the neural retina such as retinitis
 CC pigmentosa, drug-induced retinopathies, stationary forms of night
 CC blindness, progressive cone-rod degeneration, immune disorders and
 CC hematopoietic disorders. (I) is effective in treating neurological
 CC conditions and promotes neuron regeneration. Neural functions are
 CC effectively restored in patients suffering from various neurological
 CC disorders. This sequence encodes the human NNT-1 protein described in the
 CC method of the invention
 XX Sequence 797 BP; 139 A; 297 C; 218 G; 143 T; 0 U; 0 Other;
 SQ Query Match 10.3%; Score 523.4; DB 3; Length 797;
 Best Local Similarity 99.8%; Pred. No. 2.9e-119;
 Matches 524; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 3363 AGCTGAAGTACCTGGGCCCCCTTTCAAGAGCCAGACTTCAACCTCCCGCCCTGGGG 3422
 DB 271 ATCTGAAGTACCTGGGCCCCCTTTCAAGAGCCAGACTTCAACCTCCCGCCCTGGGG 330
 QY 3423 CAGAGACTTGCCCGAGGGCCACTGTGTACTTGGAGGTGGGGAAGCTCAATGACAAAC 3482
 DB 331 CAGAGACTTGCCCGAGGGCCACTGTGTACTTGGAGGTGGGGAAGCTCAATGACAAAC 390
 QY 3483 TCGCGGTGACCCAGAGACTACAGGGCCCTACAGCCACTTCTGTGTACTTGGTGGCTCA 3542
 DB 391 TCGCGGTGACCCAGAGACTACAGGGCCCTACAGCCACTTCTGTGTACTTGGTGGCTCA 450

QY 3543 ACCGTGAGGCTGCCACTGTGAGCTGCGCGCGAGCTGGCCCACTTCTGCACCAAGCTCC 3602
 DB 451 ACCGTGAGGCTGCCACTGTGAGCTGCGCGCGAGCTGGCCCACTTCTGCACCAAGCTCC 510
 QY 3603 AGGGCTGCTGGGCGAGCATTTGGGGCGCTCATGGGAGCTCTGGGCTACCCACTGCCCCAGC 3662
 DB 511 AGGGCTGCTGGGCGAGCATTTGGGGCGCTCATGGGAGCTCTGGGCTACCCACTGCCCCAGC 570
 QY 3663 CGCTGCTGGGACTGAACCCACTTGGACTTCTTGGGCGCTGGCCACAGTGAATTCCTCCAGA 3722
 DB 571 CGCTGCTGGGACTGAACCCACTTGGACTTCTTGGGCGCTGGCCACAGTGAATTCCTCCAGA 630
 QY 3723 AGATGAGAGACTTCTGGGCTGTAAGAGGAGCTGCAGACCTGGTGTGGCGCTGGGCAAGG 3782
 DB 631 AGATGAGAGACTTCTGGGCTGTAAGAGGAGCTGCAGACCTGGTGTGGCGCTGGGCAAGG 690
 QY 3783 ACTTCAACCGGCTCAAGAGAGAGTGCAGGCTCCAGAGAGTGCAGTCAACCTTGCACTGG 3842
 DB 691 ACTTCAACCGGCTCAAGAGAGAGTGCAGGCTCCAGAGAGTGCAGTCAACCTTGCACTGG 750
 QY 3843 GGGCTCATGGCTTCTGACTTCTGACTTCTGACTTCTGCTCTCTGCTGCTGCTGCTGCTG 3887
 DB 751 GGGCTCATGGCTTCTGACTTCTGACTTCTGACTTCTGCTCTCTGCTGCTGCTGCTGCTG 795
 RESULT 13
 ABX11647
 ID ABK11647 standard; cDNA; 797 BP.
 XX AC ABK11647;
 XX DT 05-JUN-2002 (first entry)
 XX DE Human cDNA encoding novel neurotrophic factor NNT1.
 XX Human; ss; Gene; NNT1; neurotrophic factor; IGE-related disease;
 KW Type I allergic disease; allergic rhinitis; eczema; dermatitis;
 KW pollinosis; asthma; immune disease; cancer; arteriosclerosis;
 KW vascular restenosis; rheumatoid arthritis; psoriatic arthritis;
 KW inflammatory arthritis; osteoarthritis; inflammatory joint disease;
 KW autoimmune disease; multiple sclerosis; lupus; diabetes; endometriosis;
 KW inflammatory bowel disease; transplant rejection; reproductive disorder;
 KW graft versus host disease; infertility; miscarriage; preterm labour.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 FH CDS 90..767
 FT /*tag= a
 FT /product= "NNT1"
 XX W0200215977-A2.
 XX 28-FEB-2002.
 XX 17-AUG-2001; 2001WO-US025906.
 XX 18-AUG-2000; 2000US-0226436P.
 XX 18-AUG-2001; 2001US-00931704.
 XX (AMGE-) AMGEN INC.
 XX Senaldi G;
 XX WPI; 2002-280867/32.
 XX P-PSDB; AAU78116.
 XX Treating Immunoglobulin E-related disease, modulating IgE levels in a
 PT patient, preventing IGE-related disease and treating allergic diseases,
 PT involves administering NNT-1 inhibitor to a patient.
 XX Claim 2; Fig 1; 63pp; English.

XX CC The invention relates to treating Immunoglobulin E (IgE)-related disease, modulating IgE levels in a patient, preventing an IgE-related disease, and treating allergic diseases, comprising administering a therapeutically effective amount of novel neurotrophic factor (NNT)-1 inhibitor to a patient. Also included are a method of diagnosing an IgE-related disease or susceptibility to an IgE-related disease, by determining the presence or amount of expression of an NNT1 polypeptide encoded by a NNT1 nucleotide sequence, its fragment or naturally occurring variant, and diagnosing an IgE-related disease or susceptibility of an IgE-related disease based on the presence or amount of expression of the polypeptide and a pharmaceutical composition for use in treating IgE-related disease, comprising the NNT1 inhibitor. The NNT1 inhibitor is useful for preventing and treating IgE-related disease, modulating IgE levels, and treating allergic diseases e.g. Type I allergic disease, allergic rhinitis, eczema, dermatitis, pollinosis, asthma, immune diseases and disorders, diseases involving abnormal cell proliferation including cancer, arteriosclerosis and vascular restenosis, diseases and conditions relating to dysfunction of immune system including rheumatoid arthritis, psoriatic arthritis, inflammatory arthritis, osteoarthritis, inflammatory joint disease, autoimmune disease, multiple sclerosis, lupus, diabetes, inflammatory bowel disease, transplant rejection, and graft versus host disease, and reproductive diseases and disorders including infertility, miscarriage, preterm labour and delivery, and endometriosis. The present sequence encodes human NNT1

XX SQ Sequence 797 BP; 139 A; 297 C; 218 G; 143 T; 0 U; 0 Other;

Query Match 10.3%; Score 523.4; DB 6; Length 797;
 Best Local Similarity 99.8%; Pred. NO. 2.9e-119;
 Matches 524; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3363 AGCTGAACCTACCTGGGCCCCCTTCAACGAGCAGACTCAACCTCCGCCCTGGGGG 3422
 DB 271 ATCTGAACCTACCTGGGCCCCCTTCAACGAGCAGACTCAACCTCCGCCCTGGGGG 330

QY 3423 CAGAGACTCTGCCAGGGCCACTGTGTGATTGGAGGTGGCGAAGCTCAATGACAAAC 3482
 DB 331 CAGAGACTCTGCCAGGGCCACTGTGTGATTGGAGGTGGCGAAGCTCAATGACAAAC 390

QY 3483 TGGGGCTGACCCAGACTACGAGGCTCAGACCCCTCTGTTACTTGGCTGGCCCTCA 3542
 DB 391 TGGGGCTGACCCAGACTACGAGGCTCAGACCCCTCTGTTACTTGGCTGGCCCTCA 450

QY 3543 ACCGTGAGGCTGACCTGCTGAGCTGCGCGCGAGCCTGGCCCACTTGTGACAGCCCTCC 3602
 DB 451 ACCGTGAGGCTGACCTGCTGAGCTGCGCGCGAGCCTGGCCCACTTGTGACAGCCCTCC 510

QY 3603 AGGGCTGTGGGACACATGGGGCGTCAATGGAGCTTGGGCTACCCACTGGCCCGAGC 3662
 DB 511 AGGGCTGTGGGACACATGGGGCGTCAATGGAGCTTGGGCTACCCACTGGCCCGAGC 570

QY 3663 CGCTGCTGGGACTGAACCCACTTGGACTCTGGCCCTGCCACAGTACTTCTCTCCAGA 3722
 DB 571 CGCTGCTGGGACTGAACCCACTTGGACTCTGGCCCTGCCACAGTACTTCTCTCCAGA 630

QY 3723 AGATGACACATCTGGCTGTGAAGAGCTGAGACCTGGCTGTGGGCTCGGCCAAGG 3782
 DB 631 AGATGACACATCTGGCTGTGAAGAGCTGAGACCTGGCTGTGGGCTCGGCCAAGG 690

QY 3783 ACTTCAACCGGCTCAAGAGAGAGATGACGCTTCCAGAGCTGACCTGACCTGACCTGG 3842
 DB 691 ACTTCAACCGGCTCAAGAGAGAGATGACGCTTCCAGAGCTGACCTGACCTGACCTGG 750

QY 3843 GGCTCATGGCTTCTGACTTCTGACTTCTCTCTTGGCTCCCCC 3887
 DB 751 GGCTCATGGCTTCTGACTTCTGACTTCTCTCTTGGCTCCCCC 795

RESULT 14

ABA09140

ID ABA09140 standard; cDNA; 968 BP.

XX

AC ABA09140;
 XX 11-JAN-2002 (first entry)
 XX Human cardiostrophin-like cytokine homologue cDNA, SEQ ID NO:916.
 XX Human; cytokine; cell proliferation; cell differentiation; growth factor;
 KW haematopoiesis regulation; tissue growth; immunomodulator; activin;
 KW inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
 KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
 KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
 KW chronic inflammatory condition; proliferative retinopathy;
 KW atherosclerosis; coronary heart disease; arterial ischaemia;
 KW bone disorder; osteoporosis; vascular growth disorder;
 KW tissue regeneration; wound healing; infection; immune disorder;
 KW cell culture; drug screening; gene therapy; antiinflammatory;
 KW antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
 KW cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
 KW antifungal; vulnary; antiulcer; ss.
 XX Homo sapiens.
 OS WO200157198-A2.
 XX 09-AUG-2001.
 XX 05-FEB-2001; 2001WO-US003800.
 XX 03-FEB-2000; 2000US-00496914.
 PR 27-APR-2000; 2000US-00560875.
 XX (HYSE-) HYSEQ INC.
 PA Tang YT, Liu C, Drmanac RT;
 PI WPI; 2001-457740/49.
 DR P-ESDE; ABB11896.
 XX Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject e.g. arthritis and cancer.
 Claim 1; Page 793-794; 1963pp; English.
 XX Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA08225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of detecting the nucleotides or polypeptides in a sample, and methods of identifying compounds which bind to polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may have various activities, including cytokine, cell proliferation or cell differentiation activities; stem cell growth factor activity; haematopoiesis regulatory activity; tissue growth activity; immunomodulatory activity; activin- or inhibin-related activities; chemotactic or chemokinetic activities; haemostatic, thrombotic or thrombolytic activities; receptor or ligand activities; or may be involved in oncogenesis, cancer cell proliferation or metastasis. Depending on their biological activities, polypeptides and nucleotides of the invention are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Such conditions include cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell disorders), chronic inflammatory conditions (e.g., asthma or arthritis), proliferative retinopathy, atherosclerosis, coronary heart disease, arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal vascular growth. Polypeptides involved with tissue regeneration and repair (or nucleic acids encoding them) may be used to promote wound healing (e.g., of burns, incisions and ulcers), while those with immunomodulatory activities may be used in the treatment of viral, bacterial and fungal infections in addition to immune disorders.

CC Polypeptides with growth factor activity may be used in cell cultures to
CC promote cell growth. For example, such polypeptides may be used to
CC manipulate stem cells in culture to give rise to neuroepithelial cells
CC that can be used to augment or replace cells damaged by illness,
CC autoimmune disease or accidental damage. The polypeptides and nucleotides
CC may also be used in the diagnosis of the above conditions, and in drug
CC screening techniques. The present sequence represents a cDNA encoding a
CC novel human polypeptide of the invention

XX
SQ Sequence 968 BP; 179 A; 353 C; 244 G; 192 T; 0 U; 0 Other;
Query Match 9.7%; Score 495.4; DB 4; Length 968;
Best Local Similarity 99.8%; Pred. No. 2.8e-112;
Matches 496; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3363 AGCTGAACCTACTGGGCCCCCTTTCAACAGAGCAGACTTCAACCTCCCGCTGGGG 3422
Db 472 ATCTGAACCTACTGGGCCCCCTTTCAACAGAGCAGACTTCAACCTCCCGCTGGGG 531
QY 3423 CAGAGACTCTGCCAGGGCCACTGTGACTTGGAGGTGTGGGAAGCTCAATGACAAAC 3482
Db 532 CAGAGACTCTGCCAGGGCCACTGTGACTTGGAGGTGTGGGAAGCTCAATGACAAAC 591
QY 3483 TGGCGCTGACCCAGAACTACGAGGCTACAGCCACCTTCTGTGTACTTGGTGGCTCA 3542
Db 592 TGGCGCTGACCCAGAACTACGAGGCTACAGCCACCTTCTGTGTACTTGGTGGCTCA 651
QY 3543 ACCGTGAGCTGACCTGCTGAGCTGGCGCCAGCTGGCCACTTCTGACAGGCTCC 3602
Db 652 ACCGTGAGCTGACCTGCTGAGCTGGCGCCAGCTGGCCACTTCTGACAGGCTCC 711
QY 3603 AGGGCTCTGGGAGCACTTGGGCGCTGTCAGGAGCTCTGGGCTACCCACTGCCCAGC 3662
Db 712 AGGGCTCTGGGAGCACTTGGGCGCTGTCAGGAGCTCTGGGCTACCCACTGCCCAGC 771
QY 3663 CGCTGCTGGAGCTGAACCACTTGGACTCTGGCCCTGCCACAGTACTTCTCCAGA 3722
Db 772 CGCTGCTGGAGCTGAACCACTTGGACTCTGGCCCTGCCACAGTACTTCTCCAGA 831
QY 3723 AGATGACGACTCTGGCTGTGAGGAGCTGACAGCTGTGGGCTCGGCCAAGG 3782
Db 832 AGATGACGACTCTGGCTGTGAGGAGCTGACAGCTGTGGGCTCGGCCAAGG 891
QY 3783 ACTTCAACCGGCTCAAGAAGAGATGACGCTTCCAGAGCTGCAGTCAACCTGACCTGG 3842
Db 892 ACTTCAACCGGCTCAAGAAGAGATGACGCTTCCAGAGCTGCAGTCAACCTGACCTGG 951
QY 3843 GGGCTCATGGCTTCTGA 3859
Db 952 GGGCTCATGGCTTCTGA 968

RESULT 15
AAK52532
ID AAK52532 standard; cDNA; 968 BP.
XX
AC AAK52532;
XX
DT 06-NOV-2001. (first entry)
XX
DE Human polynucleotide SEQ ID NO 2061.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation; ss.
XX
OS Homo sapiens.
XX
FN WO200157190-A2.
XX
PD 09-AUG-2001.
XX

PF 05-FEB-2001; 2001WO-US004098.
XX
PR 03-FEB-2000; 2000US-00496914.
PR 27-APR-2000; 2000US-00560875.
PR 20-JUN-2000; 2000US-00598075.
PR 19-JUL-2000; 2000US-00620325.
PR 01-SEP-2000; 2000US-00654936.
PR 15-SEP-2000; 2000US-00663561.
PR 20-OCT-2000; 2000US-00693325.
PR 30-NOV-2000; 2000US-00728422.
XX (HYSE-) HYSEQ INC.
PA
XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
PI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejman I, Goodrich R;
XX
DR WPI; 2001-476283/51.
DR P-PSDB; AAM79399.
XX
PT Nucleic acids encoding polypeptides with cytokine-like activities, useful
PT in diagnosis and gene therapy.
XX
PS Claim 1; Page 4448-4448; 6221pp; English.
XX
PS The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
CC (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
CC sequence listing were missing at the time of publication
XX
SQ Sequence 968 BP; 179 A; 353 C; 244 G; 192 T; 0 U; 0 Other;

Query Match 9.7%; Score 495.4; DB 4; Length 968;
Best Local Similarity 99.8%; Pred. No. 2.8e-112;
Matches 496; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3363 AGCTGAACCTACTGGGCCCCCTTTCAACAGAGCAGACTTCAACCTCCCGCTGGGG 3422
Db 472 ATCTGAACCTACTGGGCCCCCTTTCAACAGAGCAGACTTCAACCTCCCGCTGGGG 531
QY 3423 CAGAGACTCTGCCAGGGCCACTGTGACTTGGAGGTGTGGGAAGCTCAATGACAAAC 3482
Db 532 CAGAGACTCTGCCAGGGCCACTGTGACTTGGAGGTGTGGGAAGCTCAATGACAAAC 591
QY 3483 TGGCGCTGACCCAGAACTACGAGGCTTACAGCCACCTTCTGTGTACTTGGTGGCTCA 3542
Db 592 TGGCGCTGACCCAGAACTACGAGGCTTACAGCCACCTTCTGTGTACTTGGTGGCTCA 651
QY 3543 ACCGTGAGCTGACCTGCTGAGCTGGCGCCAGCTGGCCACTTCTGACAGCAGCTCC 3602
Db 652 ACCGTGAGCTGACCTGCTGAGCTGGCGCCAGCTGGCCACTTCTGACAGCAGCTCC 711
QY 3603 AGGGCTCTGGGAGCACTTGGGCGCTGTCAGGAGCTCTGGGCTACCCACTGCCCAGC 3662
Db 712 AGGGCTCTGGGAGCACTTGGGCGCTGTCAGGAGCTCTGGGCTACCCACTGCCCAGC 771
QY 3663 CGCTGCTGGAGCTGAACCACTTGGACTCTGGCCCTGCCACAGTACTTCTCCAGA 3722
Db 772 CGCTGCTGGAGCTGAACCACTTGGACTCTGGCCCTGCCACAGTACTTCTCCAGA 831
QY 3723 AGATGACGACTCTGGCTGTGAGGAGCTGACAGCTGTGGGCTCGGCCAAGG 3782
Db 832 AGATGACGACTCTGGCTGTGAGGAGCTGACAGCTGTGGGCTCGGCCAAGG 891

Qy	3783	ACTTCAACCGGCTCAAGAGAGATGAGCTCCAGCAGCTGCAGTCAACCTGCACCTGG	3842
Db	892	ACTTCAACCGGCTCAAGAGAGATGAGCTCCAGCAGCTGCAGTCAACCTGCACCTGG	951
Qy	3843	GGGCTCATGGCTTCTGA	3859
Db	952	GGGCTCATGGCTTCTGA	968

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OM nucleic - nucleic search, using sw model

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- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:
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- 19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5087	100.0	5087	9	US-09-931-704-3
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3	735.4	14.5	809	13	US-10-027-632-134702
4	735.4	14.5	809	15	US-10-027-632-134702
5	630.6	12.4	631	13	US-10-027-632-134703
6	630.6	12.4	631	13	US-10-027-632-134704
7	630.6	12.4	631	16	US-10-027-632-134703
8	630.6	12.4	631	16	US-10-027-632-134704
9	523.4	10.3	797	9	US-09-931-704-1
10	495.4	9.7	968	13	US-10-276-774-916
c 11	493.4	9.7	495	9	US-09-864-761-23175
c 12	492.4	9.7	768	13	US-10-296-115-607
c 13	492	9.7	492	9	US-09-864-761-6462
14	437.2	8.6	465	9	US-09-867-701-4667

15	429.6	8.4	819	9	US-09-931-704-4
c 16	429.4	8.4	432	9	US-09-867-701-4636
c 17	398	7.8	457	10	US-09-918-935-9935
c 18	355.8	7.0	360	9	US-09-867-701-2610
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20	250.6	4.9	269	9	US-09-867-701-5382
21	192.8	3.8	231	9	US-09-867-701-2639
22	165.2	3.2	283	9	US-09-765-231A-75
23	70.8	1.4	2750	13	US-09-854-867-362
24	66.8	1.3	12050	17	US-10-300-820-4
25	60	1.2	60	10	US-09-908-975-14602
26	60	1.2	60	10	US-09-908-975-32089
27	60	1.2	60	10	US-09-908-975-32301
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c 29	58.6	1.2	65	10	US-09-908-975-29446
c 30	58.6	1.2	28055	16	US-10-085-117-94
c 31	57.8	1.1	2778	17	US-10-437-963-56837
c 32	57.8	1.1	5452	15	US-10-017-161-1481
c 33	57.6	1.1	5452	16	US-10-292-798-1189
c 34	57.6	1.1	53522	10	US-09-904-968A-1
c 35	56	1.1	186391	13	US-10-087-132-136
c 36	54.4	1.1	1064	9	US-09-804-682-29
c 37	54.2	1.1	574	13	US-10-027-632-139721
c 38	54.2	1.1	574	16	US-10-027-632-139721
c 39	54	1.1	571	15	US-10-184-644-346
c 40	54	1.1	671	15	US-10-184-634-346
c 41	54	1.1	1239	17	US-10-332-859-215
c 42	53.8	1.1	594	13	US-10-142-426-10
c 43	53.8	1.1	594	15	US-10-123-155-10
c 44	53.8	1.1	594	15	US-10-146-731-10
c 45	53.8	1.1	594	15	US-10-140-472-10

ALIGNMENTS

RESULT 1

US-09-931-704-3
; Sequence 3, Application US/09931704
; Patent No. US20020041873A1
; GENERAL INFORMATION:
; APPLICANT: Senaldi, Giorgio
; TITLE OF INVENTION: Methods and Compositions for Treating IgE-Related Disease Using N
; TITLE OF INVENTION: Inhibitors
; FILE REFERENCE: A-695
; CURRENT APPLICATION NUMBER: US/09/931,704
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: US 60/226,436
; PRIOR FILING DATE: 2000-08-18
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 5087
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (137)..(138)
; OTHER INFORMATION: product = "INTERVENING UNSEQUENCED REGION OF >1KB"
US-09-931-704-3

Query Match	100.0%	Score 5087	DB 9	Length 5087
Best Local Similarity	100.0%	Pred. No. 0		
Matches 5087	Conservative	0	Mismatches	0
		0	Indels	0
		0	Gaps	0
Qy	1	AACTCGGAGTGGCGCTCGCGGATGGGATTAAAGCTTCGCGGAGCGCGGCTCGGC	60	
Db	1	AACTCGGAGTGGCGCTCGCGGATGGGATTAAAGCTTCGCGGAGCGCGGCTCGGC	60	
Qy	61	CTCCCACTCGCGAGCCTCGCGGAGGAGCGCACCGCGCGCCAGCCAGCCCCA	120	
Db	61	CTCCCACTCGCGAGCCTCGCGGAGGAGCGCACCGCGCGCCAGCCAGCCCCA	120	

Qy	121	TGGACCTCGAGCAGGTTGAAAAACCCAAACCTAGCCCTGCTCTTCATAAACATGACAAGCAG	180
Db	121	TGGACCTCCGAGCAGGTTGAAAAACCCAAACCTAGCCCTGCTCTTCATAAACATGACAAGCAG	180
Qy	181	CGCCCCATCTGATACCTAAACCGGACCAAGTCACAGCCCTCAACTCACCTCTGCGCTGCC	240
Db	181	CGCCCCATCTGATACCTAAACCGGACCAAGTCACAGCCCTCAACTCACCTCTGCGCTGCC	240
Qy	241	CAGACCTCAACACATCCTTGTGGACTCAAAACCTCAACCGCACTAAATCAACCAAAATCCCA	300
Db	241	CAGACCTCAACACATCCTTGTGGACTCAAAACCTCAACCGCACTAAATCAACCAAAATCCCA	300
Qy	301	AGCTCAACTAATCTGAAACTTTTAAAGTAACCCAGTCCTTAAACCTAAACCTAGCCCAAT	360
Db	301	AGCTCAACTAATCTGAAACTTTTAAAGTAACCCAGTCCTTAAACCTAAACCTAGCCCAAT	360
Qy	361	GCCAAATATATCTAACCTAGCCAAACCTCAACTGCCCTTGCAGTCCAAAGTGTCCACTG	420
Db	361	GCCAAATATATCTAACCTAGCCAAACCTCAACTGCCCTTGCAGTCCAAAGTGTCCACTG	420
Qy	421	AATCCTCACCTTGTCTCTCACTGAAATCCGAGAAAGCATATTTCCCACTGCCACAT	480
Db	421	AATCCTCACCTTGTCTCTCACTGAAATCCGAGAAAGCATATTTCCCACTGCCACAT	480
Qy	481	CCCTCCCTTACAGACCCAAACCTCGGCTCTGGACTCCTGGTATCCTGGGATGTCCAAACT	540
Db	481	CCCTCCCTTACAGACCCAAACCTCGGCTCTGGACTCCTGGTATCCTGGGATGTCCAAACT	540
Qy	541	CTGCAGTGCATCAGCAACAGCCCGAATGCTCAAAATGCACTCTCTCCCTCTCTGTCC	600
Db	541	CTGCAGTGCATCAGCAACAGCCCGAATGCTCAAAATGCACTCTCTCCCTCTCTGTCC	600
Qy	601	CCACCTTGAGGCTGATGGAAGGCGCTCATGGAAGTCCAACTTTCCCACTTAACACC	660
Db	601	CCACCTTGAGGCTGATGGAAGGCGCTCATGGAAGTCCAACTTTCCCACTTAACACC	660
Qy	661	AAGAACGGGTGAACCTCCACACTGCCACCGTTCCTGAGAGTGAGCACTAAATCTCCTT	720
Db	661	AAGAACGGGTGAACCTCCACACTGCCACCGTTCCTGAGAGTGAGCACTAAATCTCCTT	720
Qy	721	CAATCTAACCCACCTACACTTCCGACCTCAGGAATCACTCTAGATATATACCCAAA	780
Db	721	CAATCTAACCCACCTACACTTCCGACCTCAGGAATCACTCTAGATATATACCCAAA	780
Qy	781	ACTAAGCCCCATAGGCAGCCGACCTAGTGGTCTAACCTATACCTTGCCTCTCTATGG	840
Db	781	ACTAAGCCCCATAGGCAGCCGACCTAGTGGTCTAACCTATACCTTGCCTCTCTATGG	840
Qy	841	GTGAGTCTGTTCTTGGGGCGGCGCTCTCTCTGCTTCCCTTGTAGAGTGTACTGTGCTC	900
Db	841	GTGAGTCTGTTCTTGGGGCGGCGCTCTCTCTGCTTCCCTTGTAGAGTGTACTGTGCTC	900
Qy	901	AGCCTGCAGCTCTGACATGTGCTCTCCACCTCTGACTCCCTCCCTCAAGCTGCAGTGG	960
Db	901	AGCCTGCAGCTCTGACATGTGCTCTCCACCTCTGACTCCCTCCCTCAAGCTGCAGTGG	960
Qy	961	GACTGGAAGATGCGCAGAAAGCTAGGGTCAAACTGGAAACAGGCGAGGTGGACTGCGAGT	1020
Db	961	GACTGGAAGATGCGCAGAAAGCTAGGGTCAAACTGGAAACAGGCGAGGTGGACTGCGAGT	1020
Qy	1021	CCCTAGCCCTGGCCCGCTCCCTCACTGACACATATACATGTGTGSCACACACAGATG	1080
Db	1021	CCCTAGCCCTGGCCCGCTCCCTCACTGACACATATACATGTGTGSCACACACAGATG	1080
Qy	1081	GCACACATGCCAAAGACTCTCTCAGCTGACACAGATCCATTCTCAAGTATCTACTGAT	1140
Db	1081	GCACACATGCCAAAGACTCTCTCAGCTGACACAGATCCATTCTCAAGTATCTACTGAT	1140
Qy	1141	AGACACTCTGCGTGCAGTCTCTCACTCCTCAACATACACATGCTCTTTCTCTCC	1200
Db	1141	AGACACTCTGCGTGCAGTCTCTCACTCCTCAACATACACATGCTCTTTCTCTCC	1200
Qy	1201	GTCTTGGCAGGAGTGTTCCTCTCCTCATCCCTCTGCGCTGCCATCTGGTGTCCCACT	1260

DB	1201	GTC TTG CAG AG G T TT CC C CT C CT C AT C C C CT C G C CT C C AT CT G T G T C C CA CC C	1260
QY	1261	TC AC CC CC CC CA CC CA G G T G G G G CA G A C A C CT G A G G G G T G C C A G T G CT T C C C	1320
DB	1261	TC AC CC CC CC CA CC CA G G T G G G G CA G A C A C CT G A G G G G T G C C A G T G CT T C C C	1320
QY	1321	GT GT G G G G C G G G C G G C T A G C T T C G T C C AT C T G T C C CA C A G G G A C T G T G G G	1380
DB	1321	GT GT G G G G C G G G C G G C T A G C T T C G T C C AT C T G T C C CA C A G G G A C T G T G G G	1380
QY	1381	G AT CT T A G C G T G C T G C A G G T G T G G C A C CT C C T G C A G T G C A G T C T C A AT C G	1440
DB	1381	G AT CT T A G C G T G C T G C A G G T G T G G C A C CT C C T G C A G T G C A G T C T C A AT C G	1440
QY	1441	C A G G G G A C C C A G G G C T G G C C C T C C AT C C A G A A A C CT A T G A C T C A C C G C T A C CT	1500
DB	1441	C A G G G G A C C C A G G G C T G G C C C T C C AT C C A G A A A C CT A T G A C T C A C C G C T A C CT	1500
QY	1501	G G A C C A C A C T C G C A G C T T G C T G G A C C T A T G A G T A T C A G C G T A G G A A C T G G G	1560
DB	1501	G G A C C A C A C T C G C A G C T T G C T G G A C C T A T G A G T A T C A G C G T A G G A A C T G G G	1560
QY	1561	A G T T G G G G A G T G A G A G T T G G G A A A C A G T C T A A C C G T G A G G T T C T G T A A	1620
DB	1561	A G T T G G G G A G T G A G A G T T G G G A A A C A G T C T A A C C G T G A G G T T C T G T A A	1620
QY	1621	T G A T G G G T G A G A G G G C T T T T G C T C C A C A G T C C C C T G T C T G T C T A T C C C T G	1680
DB	1621	T G A T G G G T G A G A G G G C T T T T G C T C C A C A G T C C C C T G T C T G T C T A T C C C T G	1680
QY	1681	C C T T C C C T C T A G T G G C C C C C C C A C T T C C C C A T C C T G G C C C A G A C T A G C A T G T	1740
DB	1681	C C T T C C C T C T A G T G G C C C C C C C A C T T C C C C A T C C T G G C C C A G A C T A G C A T G T	1740
QY	1741	G G C A G G C T G C A C C G C C T T G G C C A T T G C C C A C A G T G C C C C A G C C A G C C G C G C	1800
DB	1741	G G C A G G C T G C A C C G C C T T G G C C A T T G C C C A C A G T G C C C C A G C C A G C C G C G C	1800
QY	1801	T C C C C T G G G G C G G G A G T C C T C T G T T A C C G T G T G T G T C T G T C T G C G	1860
DB	1801	T C C C C T G G G G C G G G A G T C C T C T G T T A C C G T G T G T G T C T G T C T G C G	1860
QY	1861	G G C G G G T G G T G G G A C A G A G G G C C C A C T C C A T G C T G G T T C A G T C G C T C	1920
DB	1861	G G C G G G T G G T G G G A C A G A G G G C C C A C T C C A T G C T G G T T C A G T C G C T C	1920
QY	1921	T G C C C C C A G A C C T G G G C C T G T C T G G A C C C A G G G C C C C T C C T C C G T C T G C T C	1980
DB	1921	T G C C C C C A G A C C T G G G C C T G T C T G G A C C C A G G G C C C C T C C T C C G T C T G C T C	1980
QY	1981	C C A T C C T A G C T G G G C C C T A G G G G G T C A T G G G A A G G G A C T G T A G G A A C C A G G	2040
DB	1981	C C A T C C T A G C T G G G C C C T A G G G G G T C A T G G G A A G G G A C T G T A G G A A C C A G G	2040
QY	2041	C A G T G G C A G G G G T T A G G T G G A T G A G G T T A G C T G T A G G A T T T G G G G T G	2100
DB	2041	C A G T G G C A G G G G T T A G G T G G A T G A G G T T A G C T G T A G G A T T T G G G G T G	2100
QY	2101	T C C A G A G G T T C A G A G C C C A G A G A A G A G G G T T G A G G A G C C C A G G C C A G G C C	2160
DB	2101	T C C A G A G G T T C A G A G C C C A G A G A A G A G G G T T G A G A G C C C A G G C C A G G C C	2160
QY	2161	A T G G G A A C G G C C C C T T C C G T G T C T T C C A T C C C A G A C C T A C T C T	

Qy	4501	ACCCGAGCTGAGCATCAGGACCTTGCTCGAAATTGCTTCCAGTAATTACGGTGCCTCTTC	4560
Db	4501	ACCCGAGCTGAGCATCAGGACCTTGCTCGAAATTGCTTCCAGTAATTACGGTGCCTCTTC	4560
Qy	4561	TCTGCCCCCTTTCCAGGGTATCTGTGGGTTCGCCAGCTGGGAGGGCAACATAGCCAC	4620
Db	4561	TCTGCCCCCTTTCCAGGGTATCTGTGGGTTCGCCAGCTGGGAGGGCAACATAGCCAC	4620
Qy	4621	ACCACAGGATTTCTCTGAAAGTTTACAAATGCAGTAGCAATTTGGGGTGTAGGGTGGCAGCT	4680
Db	4621	ACCACAGGATTTCTCTGAAAGTTTACAAATGCAGTAGCAATTTGGGGTGTAGGGTGGCAGCT	4680
Qy	4681	CCCCAAGGCCCTGCCCCAGCCGCCACCCACTCATGACTCTAAAGTGTTGTTAATTAAT	4740
Db	4681	CCCCAAGGCCCTGCCCCAGCCGCCACCCACTCATGACTCTAAAGTGTTGTTAATTAAT	4740
Qy	4741	TTATTTATTTGGAGATGTTATTTATTAGATGATATTTATTGCAGAAATTTCTATCTTGTA	4800
Db	4741	TTATTTATTTGGAGATGTTATTTATTAGATGATATTTATTGCAGAAATTTCTATCTTGTA	4800
Qy	4801	TTAAACAATAAATGCTTGGCCCAAGAACTTAGTGCTCTTTGCCACAGCCTCACCCCTCCTGG	4860
Db	4801	TTAAACAATAAATGCTTGGCCCAAGAACTTAGTGCTCTTTGCCACAGCCTCACCCCTCCTGG	4860
Qy	4861	TGCTCATCAGACTCTTGCCACCCCTGGCTCCCACTCCCTGCTTGCCCTCTGGTGGAGTGC	4920
Db	4861	TGCTCATCAGACTCTTGCCACCCCTGGCTCCCACTCCCTGCTTGCCCTCTGGTGGAGTGC	4920
Qy	4921	ACAGAGCTCTGGGAAGAGGGCCCTTCTCCCTCCCGCACTGGGGCGATGGGCGACCTCAGA	4980
Db	4921	ACAGAGCTCTGGGAAGAGGGCCCTTCTCCCTCCCGCACTGGGGCGATGGGCGACCTCAGA	4980
Qy	4981	CTTACCACACTGCTGCTGCCACCAACCAACCCCTTGATCCCTCAGTCTCTCCACACAGCTTC	5040
Db	4981	CTTACCACACTGCTGCTGCCACCAACCAACCCCTTGATCCCTCAGTCTCTCCACACAGCTTC	5040
Qy	5041	TGTCACACCCAGGTTTCCCTCAACCCACACCTTTGCTAAGTCTTCCTCA	5087
Db	5041	TGTCACACCCAGGTTTCCCTCAACCCACACCTTTGCTAAGTCTTCCTCA	5087

RESULT 2

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US-10-212-793-1
; Sequence 1, Application US/10212793
; Publication No. US20030087395A1
; GENERAL INFORMATION:
; APPLICANT: Shi et al.
; TITLE OF INVENTION: Cardiotrophin-Like Cytokine
; FILE REFERENCE: PF385D1C1
; CURRENT APPLICATION NUMBER: US/10/212,793
; CURRENT FILING DATE: 2003-08-07
; PRIOR APPLICATION NUMBER: US 09/438,299
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 09/106,182
; PRIOR FILING DATE: 1998-06-29
; PRIOR APPLICATION NUMBER: US 60/051,311
; PRIOR FILING DATE: 1997-06-30
; NUMBER OF SEQ ID NOS: 24
; SEQ ID NO 1
; LENGTH: 1710
; TYPE: DNA
; ORGANISM: homo sapiens
; FEATURE:
; LOCATION: CDS
; OTHER INFORMATION: (46)..(720)
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (46)..(126)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (127)..(720)
US-10-212-793-1

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Query Match	28.8%;	Score 1463.4;	DB 15;	Length 1710;
Best Local Similarity	99.9%;	Pred. No. 0;		
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			Indels	0;
			Gaps	0;
QY	3363	AGCTGAACCTACCTGGGCCCCCTTTCAAAGAGCGACAGATTCAACCTCTCCCGCTGGGGG	3422	
DB	227	ATCTGAACCTACCTGGGCCCCCTTTCAAAGAGCGACAGATTCAACCTCTCCCGCTGGGG	286	
QY	3423	CAGAGACTCTGCCCAGGGCCACTTGTTCAGATTGGAGGTGTGGGAGAGCTCAATGACAAAC	3482	
DB	287	CAGAGACTCTGCCCAGGGCCACTTGTTCAGATTGGAGGTGTGGGAGAGCTCAATGACAAAC	346	
QY	3483	TGGCGCTGACCCAGAACTACGAGGCTTACAGCCACCTTCGTGTACTTCGCTGGGCTCA	3542	
DB	347	TGGCGCTGACCCAGAACTACGAGGCTTACAGCCACCTTCGTGTACTTCGCTGGGCTCA	406	
QY	3543	ACCGTCAGGCTGCCACTTGCTGAGCTGCGCGCAGCCTGGCCCACTTCTGACCAAGCTCC	3602	
DB	407	ACCGTCAGGCTGCCACTTGCTGAGCTGCGCGCAGCCTGGCCCACTTCTGACCAAGCTCC	466	
QY	3603	AGGCGCTGCTGGGCAGCATTTGCGGGGCTCATGCGAGCTCTGGGCTACCCACTGCCCAGC	3662	
DB	467	AGGCGCTGCTGGGCAGCATTTGCGGGGCTCATGCGAGCTCTGGGCTACCCACTGCCCAGC	526	
QY	3663	CGCTGCTGGGACTGAACCCACTTTGACCTCTCGCCCTGCCACAGTGAATTCTCTCCAGA	3722	
DB	527	CGCTGCTGGGACTGAACCCACTTTGACCTCTCGCCCTGCCACAGTGAATTCTCTCCAGA	586	
QY	3723	AGATGACGACTTCTGGCTGCTGAAGAGCTGCAGACCTGGCTGTGGCGCTGGCCCAAGG	3782	
DB	587	AGATGACGACTTCTGGCTGCTGAAGAGAGCTGCAGACCTGGCTGTGGCGCTGGCCCAAGG	646	
QY	3783	ACTTTCAACCGGCTCAAGAGAGATGACGCTCCAGAGCTGCAGTCAACCTGCACCTGG	3842	
DB	647	ACTTTCAACCGGCTCAAGAGAGATGACGCTCCAGAGCTGCAGTCAACCTGCACCTGG	706	
QY	3843	GGGCTCATGCTCTTGACTTCTGACCTTCTCCTTTTGGTCCCTTCAAAACCTGCTCC	3902	
DB	707	GGGCTCATGCTCTTGACTTCTGACCTTCTCCTTTTGGTCCCTTCAAAACCTGCTCC	766	
QY	3903	CACCTTTGTAGAGCCAGCCCTGTATGCCACACCTCTTGAGCCAGAGACAGAGCTGTG	3962	
DB	767	CACCTTTGTAGAGCCAGCCCTGTATGCCACACCTCTTGAGCCAGAGACAGAGCTGTG	826	
QY	3963	AGCCTCTGGGCCCTTCTCTTGACCGGCTGGGCGTGTGATGCGATCAGCCCTGTCTCCTCC	4022	
DB	827	AGCCTCTGGGCCCTTCTCTTGACCGGCTGGGCGTGTGATGCGATCAGCCCTGTCTCCTCC	886	
QY	4023	CACCTCCAAAGTCTACCGAGCTGGGAGGAGGTACAGTAGGCCCTGTCTCTCTGTT	4082	
DB	887	CACCTCCAAAGTCTACCGAGCTGGGAGGAGGTACAGTAGGCCCTGTCTCTCTGTT	946	
QY	4083	TCTACAGGAAGTCATGCTCGAGGAGTGTGAAGTGGTTAGGTTGTGTGACAGGCGCTCA	4142	
DB	947	TCTACAGGAAGTCATGCTCGAGGAGTGTGAAGTGGTTAGGTTGTGTGACAGGCGCTCA	1006	
QY	4143	TGGCCCTCTGCTTCTTTGCTTACCATTTGGCCAGTGCCCAACCGAGCCCTCAGGTGGACA	4202	
DB	1007	TGGCCCTCTGCTTCTTTGCTTACCATTTGGCCAGTGCCCAACCGAGCCCTCAGGTGGACA	1066	
QY	4203	TCTGAGGGCAGGGGTGAGGGGCCACCAACACATGCTTTCTGGGGTGAAGCCCTTT	4262	
DB	1067	TCTGAGGGCAGGGGTGAGGGGCCACCAACACATGCTTTCTGGGGTGAAGCCCTTT	1126	
QY	4263	GGCTGCCCACTCTCCTTTGATGGGTGTGCTCCCTTATCCCCAAATCACTCTATACATC	4322	
DB	1127	GGCTGCCCACTCTCCTTTGATGGGTGTGCTCCCTTATCCCCAAATCACTCTATACATC	1186	
QY	4323	CAATTGAGGAAACAACATGGTGGCAATCTCACAAAAGAGATGAGATTAAACAGTGCA	4382	
DB	1187	CAATTGAGGAAACAACATGGTGGCAATCTCACAAAAGAGATGAGATTAAACAGTGCA	1246	
QY	4383	GGGTGGGGTCTGCATTTGGAGGTGCCCTATAAACCCAGAGAGAAAAATCTGAAAGCACAG	4442	

Db 1247 GGGTTGGGCTGCAATGGAGTCCCTATAAACCAGAGAGAAATACTGAAAGCACAG 1306
QY 4443 GGGCAGGACACAGACACAGACCCAGAGTCTCCAAAGCACAGAGTGGCAACAAAC 4502
Db 1307 GGGCAGGACACAGACACAGACCCAGAGTCTCCAAAGCACAGAGTGGCAACAAAC 1366
QY 4503 CCGAGCTGAGCATCAGAGACCTTGCTCGAAATGCTTCCAGTATTACGGTGCTCTTCTC 4562
Db 1367 CCGAGCTGAGCATCAGAGACCTTGCTCGAAATGCTTCCAGTATTACGGTGCTCTTCTC 1426
QY 4563 TGGCCCTTTCCAGGATATCTGTGGTGGCCAGGCTGGGAGGGAACCATGACCCACAC 4622
Db 1427 TGGCCCTTTCCAGGATATCTGTGGTGGCCAGGCTGGGAGGGAACCATGACCCACAC 1486
QY 4623 CACAGGATTTCTGAAAGTTTACAAATGAGTACAGTATTTGGGGTGTAGGGTGGCAGTCC 4682
Db 1487 CACAGGATTTCTGAAAGTTTACAAATGAGTACAGTATTTGGGGTGTAGGGTGGCAGTCC 1546
QY 4683 CCAAGGCTTCCGCCCCCAGCCCCCAGCTCATGACTCTAAGTGTGTGTTAATAATTT 4742
Db 1547 CCAAGGCTTCCGCCCCCAGCCCCCAGCTCATGACTCTAAGTGTGTGTTAATAATTT 1606
QY 4743 ATTTATTTGGAGATGTTATTTATTAGATGATTTATTGAGATTTCTTATTCAGATTTCTTGTATT 4802
Db 1607 ATTTATTTGGAGATGTTATTTATTAGATGATTTATTGAGATTTCTTATTCAGATTTCTTGTATT 1666
QY 4803 AACAAATAAAATGCTTGCCCCAGAA 4827
Db 1667 AACAAATAAAATGCTTGCCCCAGAA 1691

RESULT 3

US-10-027-632-134702
; Sequence 134702, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 134702
; LENGTH: 809
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-134702

Query Match 14.5%; Score 735.4; DB 13; Length 809;
Best Local Similarity 97.3%; Pred. No. 4.3e-205;
Matches 789; Conservative 1; Mismatches 17; Indels 4; Gaps 4;
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Db 1 TGCTTCCCGGTGGGGCCGGCCGCTCATGCTTCGTCCTCCTGCCACAGGGGA 60

QY 1372 CTCGTGGGGATGTTAGCGTGTGCAACGGTGTCTTGCCACCTCCCTGCAGTGCACG 1431
Db 61 CTCGTGGGGATGTTAGCGTGTGCAACGGTGTCTTGCCACCTCCCTGCAGTGCACG 120
QY 1432 TCTCAATCCACAGGGGACCCAGGGGCTGGCCCCCTCCATCCAGAAAACCTATGACCTCAC 1491
Db 121 TCTCAATCCACAGGGGACCCAGGGGCTGGCCCCCTCCATCCAGAAAACCTATGACCTCAC 180
QY 1492 CCGCTACCTGGAGACCAACTCCGACGTTGGCTGGGACCTATGTAGTATCCAGCGTAG 1551
Db 181 CCGCTACCTGGAGACCAACTCCGACGTTGGCTGGGACCTATGTAGTATCCAGCGTAG 240
QY 1552 GAATCTGGAGTTGGGAGGAGTGTAGGAGTTGGGAAAAGACAGTCTTAACCTGGAGGT 1611
Db 241 GAATCTGGAGTTGGGAGGAGTGTAGGAGTTGGGAAAAGACAGTCTTAACCTGGAGGT 300
QY 1612 TCTGGTAAATGATGGGTGAGGAGGCTTTGGTCCACCAAGTCCCTGTCTGGTC 1671
Db 301 TCTGGTAAATGATGGGTGAGGAGGCTTTGGTCCACCAAGTCCCTGTCTGGTC 360
QY 1672 TATCTCTGCCCTTCCCTCTTAGGTGGCCCCCCCCCACTTCCCATCCCTGGCCCCAGGACT 1731
Db 361 TATCTCTGCCCTTCCCTCTTAGGTGGCCCCCCCCCACTTCCCATCCCTGGCCCCAGGACT 420
QY 1732 AGGCATGTGGGACAGGCTCGACCCGCTTGGCCCACTTGCACCACTGGCTGCCAGCCACG 1791
Db 421 AGGCATGTGGGACAGGCTCGACCCGCTTGGCCCACTTGCACCACTGGCTGCCAGCCACG 480
QY 1792 CCGCCCCGCTCCCTGGGGGCGGGGAAAGTCTCTCTCTTTACACCGTGTGTGGTGTCT 1851
Db 481 CCGCCCCGCTCCCTGGGGGCGGGGAAAGTCTCTCTCTTTACACCGTGTGTGGTGTCT 540
QY 1852 TCTTGGCGGGGCGGGTGTGGGTGGGACAGAGGGGCCCCACCTCCCATCCCTGGCGTTCCA 1911
Db 541 TCTTGGCGGGGCGGGTGTGGGTGGGACAGAGGGGCCCCACCTCCCATCCCTGGCGTTCCA 600
QY 1912 GCTCGCTCTGCCCCAGACCTTGGGCGCTGTCTGTGACCCAGGGGCGCTCCCTTCG 1971
Db 601 GCTCGCTCTGCCCCAGACCTTGGGCGCTGTCTGTGACCCAGGGGCGCTCCCTTCG 559
QY 1972 TCTGCTCTCCCATCTAGCTGGGCTCTTATGGGGGTCTATGGGGAAGGAGCTAGG 2031
Db 660 TCTGCTCTCCCATCTAGCTGGGCTCTTATGGGGGTCTATGGGGAAGGAGCTAGG 718
QY 2032 GAACCCAGCAGTGTGGCAGGGGTTAGGGTGTGGATGGAGTTATCTGTAGGATT 2091
Db 719 GAACCCA-GCAGTAGTGGCAGGGGG-TTAGGGTGTGAATGGAAGGTATCTGTAGGATTG 776
QY 2092 TGGGGGTGTGCCAGAGGTCTTCAGAGAGGCC 2122
Db 777 GGGGGGGGGCCAAAGGGGTATAAAAGGCC 807

RESULT 4

US-10-027-632-134702
; Sequence 134702, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363


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; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 134702
; LENGTH: 809
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-134702

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Query Match	14.5%	Score 735.4	DB 16	Length 809
Best Local Similarity	97.3%	Pred. No. 4.3e-205		
Matches 789	Conservative 1	Mismatches 17	Indels 4	Gaps 3
QY	1312	TGCTTCCCGGTGTGGGCGCGCGCGCTCATCTTCTCGTCCATCTCGCCACAGGGGA	1371	
DB	1	TGCTTCCCGGTGTGGGCGCGCGCGCTCATCTTCTCGTCCATCTCGCCACAGGGGA	60	
QY	1372	CTCTGGGGGATGTAGGTGCTGTGCAGGTGCTCTGGACCTCTCTGCAGTGCACG	1431	
DB	61	CTCTGGGGGATGTAGGTGCTGTGCAGGTGCTCTGGACCTCTCTGCAGTGCACG	120	
QY	1432	TCTCAATCGCACAGGGACCCAGGGCGCTGGCCCTCCATCCAGAAAACTATGACCTCAC	1491	
DB	121	TCTCAATCGCACAGGGACCCAGGGCGCWGGCCCTCCATCCAGAAAACTATGACCTCAC	180	
QY	1492	CGGTACTCTGAGCACCAACTCCGACGCTTGGCTGGAGCTATGTAGTATCCAGCGTAG	1551	
DB	181	CGGTACTCTGAGCACCAACTCCGACGCTTGGCTGGAGCTATGTAGTATCCAGCGTAG	240	
QY	1552	GAATCTGGGAGTTGGGAGAGTGAGAGTTGGGAAAGACAGTCTTAACCTGGAAGGT	1611	
DB	241	GAATCTGGGAGTTGGGAGAGTGAGAGTTGGGAAAGACAGTCTTAACCTGGAAGGT	300	
QY	1612	TCCTGTAAATCATGGGTGAGGAGGGCTCTTTGGCTCCACAGTCCCTCTGTCTGGTC	1671	
DB	301	TCCTGTAAATCATGGGTGAGGAGGGCTCTTTGGCTCCACAGTCCCTCTGTCTGGTC	360	
QY	1672	TATCTCTGCGCTTCCCTCTTAAGTGGCCCCCCCCCATCTCCCATCCCTGGCCCCAGGACT	1731	
DB	361	TATCTCTGCGCTTCCCTCTTAAGTGGCCCCCCCCCATCTCCCATCCCTGGCCCCAGGACT	420	
QY	1732	AGGCATGTGGCAGGCGCTCGCACCGCGCTTGGCCCATTCGCCCACTGGCTGCCAGCCCGAG	1791	
DB	421	AGGCATGTGGCAGGCGCTCGCACCGCGCTTGGCCCATTCGCCCACTGGCTGCCAGCCCGAG	480	
QY	1792	CGCGCGGCTCCCCCTGGGGCGGGGAAGTCTCTCTGTTTACACCGTGTGTGTGTCT	1851	
DB	481	CGCGCGGCTCCCCCTGGGGCGGGGAAGTCTCTCTGTTTACACCGTGTGTGTGTCT	540	
QY	1852	TCCTCGCGGGCGGGTGGGTGGGACAGAGGGGCCCACTCCCATCGCTGGCTTCCA	1911	
DB	541	TCCTCGCGGGCGGGTGGGTGGGACAGAGGGGCCCACTCCCATCGCTGGCTTCCA	600	
QY	1912	GCTGCGCTCTGCCCCAGACTGGGGCGCTGTGTCTGTGACCCAGGGGCTCTCCCTCCG	1971	
DB	601	GCTGCGCTCTGCCCCAGACTGGGGCGCTGTGTCTGTGACCCAGGGGCTCTCCCTCCG	659	
QY	1972	TCGTGCTCTCCCATCTTAGCTGGGCTCTCTAGGGGGGTCTATGGGGGAAAGGGGACTGTAGG	2031	
DB	660	TCGTGCTCTCCCATCTTAGCTGGGCTCTCTAGGGGGGTCTATGGGGGAAAGGGGACTGTAGG	718	
QY	2032	GNACCCAGGCTAGTGGCAGGGGTTTAGCGTGTGATGCGAGGTATGCTGTAAAGTAT	2091	
DB	719	GNACCCAGGCTAGTGGCAGGGGTTTAGCGTGTGATGCGAGGTATGCTGTAAAGTAT	776	
QY	2092	TGGGGGTGGTCCAGAGGTGTTCCAGAGGCC	2122	
DB	777	TGGGGGTGGTCCAGAGGTGTTCCAGAGGCC	807	

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RESULT 5
US-10-027-632-134703
; Sequence 134703, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 134703
; LENGTH: 631
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-134703

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Query Match.	12.4%;	Score 630.6;	DB 13;	Length 631;
Best Local Similarity	99.8%;	Pred. No. 2.8e-174;		
Matches 630;	Conservative	1;	Mismatches 0;	Indels 0;
Gaps	0;			
Qy	1909	CCAGCTCGCCTCTGCCCCCAGACCTGGGGCCCTGCTGCTCTGGACCCAGGGGGCCTCCCTT	1968	
Db	1	CCAGCTCGCCTCTGCCCCAGACCTGGGGCCCTGCTGCTCTGGACCCAGGGGGCCTCCCTT	60	
Qy	1969	CGTCTGCCTCTCCCATCTTAGCTGGGCTCTTAGAGGGGTCTATGGGGAGAGGGGACTGT	2028	
Db	61	CGGTCTGCCTCTCCCATCTTAGCTGGGCTCTTAGAGGGGTCTATGGGGAGAGGGGACTGT	120	
Qy	2029	AGGGAAACCCAGGCAGTAGTGGCAGGGGGTTTAGGGTCTGTGATGGAGGTTATGCTGTAAGG	2088	
Db	121	AGGGAAACCCAGGCAGTAGTGGCAGGGGGTTTAGGGTCTGTGATGGAGGTTATGCTGTAAGG	180	
Qy	2089	ATTTGGGGTGTCTCAGAGTGTCTCAGAGAGCCAGGAGAGAGGAGGGTCTGGAGG	2148	
Db	181	ATTTGGGGTGTCTCAGAGTGTCTCAGAGAGCCAGGAGAGAGGAGGGTCTGGAGG	240	
Qy	2149	AGCCGAGGCACCATGGGGAACCGGCCCTCTTTCCCGTGTTCCTCTTCCACATCCCAGAC	2208	
Db	241	AGCCGAGGCACCATGGGGAACCGGCCCTCTTTCCCGTGTTCCTCTTCCACATCCCAGAC	300	
Qy	2209	CCTACTCTGAGCCAGGGAAGAAAGGGAAGAGGTGGCGGGGAGCTGGCTCCAGCCC	2268	
Db	301	CCTACTCTGAGCCAGGGAAGAAAGGGAAGAGGTGGCGGGGAGCTGGCTCCAGCCC	360	
Qy	2269	CAGGATACCCGAGGAAATTAGTTGTCTGTGCTTGTGACGGTGTGAAACCTCCCCCTG	2328	
Db	361	CAGGATACCCGAGGAAATTAGTTGTCTGTGCTTGTGACGGTGTGAAACCTCCCCCTG	420	
Qy	2329	GGCCCTTGCTATCCAGGCCTCTCCCTTGCTTCTCCCTTCTTCCAGTTATACATCT	2388	
Db	421	GGCCCTTGCTATCCAGGCCTCTCCCTTGCTTCTCCCTTCTTCCAGTTATACATCT	480	
Qy	2389	CCCTCATCCCTTTTCCCTGGGCCCCAGCGCTCCCCAGGGTTGGAAAGGGCTCTGCCT	2448	
Db	481	CCCTCATCCCTTTTCCCTGGGCCCCAGCGCTCCCCAGGGTTGGAAAGGGCTCTGCCT	540	

QY 3423 CAGAGACTCTGCCAGGSCCACTGTTGACTTGGAGGTGTGGAGGCTCAATGACAAAC 3482
Db 331 CAGAGACTCTGCCAGGSCCACTGTTGACTTGGAGGTGTGGAGGCTCAATGACAAAC 390
QY 3483 TGGCGCTCAACCAAGAACTACAGAGGCTACAGCCACCTTCTGTACTTGGTGGGCTCA 3542
Db 391 TGGCGCTCAACCAAGAACTACAGAGGCTACAGCCACCTTCTGTACTTGGTGGGCTCA 450
QY 3543 ACCGTACAGCTGACACTGCTGAGCTGCGCCGAGCCTGGCCCACTTCTGACACAGCTTCC 3602
Db 451 ACCGTACAGCTGACACTGCTGAGCTGCGCCGAGCCTGGCCCACTTCTGACACAGCTTCC 510
QY 3603 AGGGCTCTCTGGGAGCACTTGGGCGCTGATGGAGCTTCTGGGTACCCACTGCCCCAGC 3662
Db 511 AGGGCTCTCTGGGAGCACTTGGGCGCTGATGGAGCTTCTGGGTACCCACTGCCCCAGC 570
QY 3663 CGCTGCTGGAGCTGAACCACTTGGACTCTGGCCCTGCCCAAGTGACTTCTCCAGA 3722
Db 571 CGCTGCTGGAGCTGAACCACTTGGACTCTGGCCCTGCCCAAGTGACTTCTCCAGA 630
QY 3723 AGATGGAGCACTTCTGGCTGCTGAAGAGCTGCAGACCTGGCTGCGGCCAAGG 3782
Db 631 AGATGGAGCACTTCTGGCTGCTGAAGAGCTGCAGACCTGGCTGCGGCCAAGG 690
QY 3783 ACTTCAACCGCTCAAGAAAGATGAGAGCTCCAGAGCTGCAGTCAACCTGCACTGG 3842
Db 691 ACTTCAACCGCTCAAGAAAGATGAGAGCTCCAGAGCTGCAGTCAACCTGCACTGG 750
QY 3843 GGGCTCATGGCTTCTGACTTCTGACCTTCTCTCTCTGCTCCCC 3887
Db 751 GGGCTCATGGCTTCTGACTTCTGACCTTCTCTCTCTGCTCCCC 795

RESULT 10

US-10-276-774-916
; Sequence 916, Application US/10276774
; Publication No. US2004005245A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang, Y, Tom et al
; TITLE OF INVENTION: NO. US20040053245A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-030
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US/10/276,774
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 2700
; SOFTWARE: Custom
; SEQ ID NO 916
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-276-774-916

Query Match 9.7%; Score 495.4; DB 13; Length 968;
Best Local Similarity 99.8%; Pred. No. 2.2e-134;
Matches 496; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3363 AGCTGAACCTACTGGGCCCCCTTTCAACAGAGCCAGACTTCAACCTCCCGCTGGGG 3422
Db 472 ATCTGAACCTACTGGGCCCCCTTTCAACAGAGCCAGACTTCAACCTCCCGCTGGGG 531
QY 3423 CAGAGACTCTGCCAGGCGCACTGTTGACTTGGAGGTGTGGAGGCTCAATGACAAAC 3482
Db 532 CAGAGACTCTGCCAGGCGCACTGTTGACTTGGAGGTGTGGAGGCTCAATGACAAAC 591
QY 3483 TGGGCTGACCCAGAACTACAGGCGCTACGCCCTTCTGTACTTGGTGGGCTCA 3542
Db 592 TGGGCTGACCCAGAACTACAGGCGCTACGCCCTTCTGTACTTGGTGGGCTCA 651
QY 3543 ACCGTACAGCTGACACTGCTGAGCTGCGCCGAGCCTGGCCCACTTCTGACACAGCCTCC 3602

Db 652 ACCGTACAGCTGACACTGCTGAGCTGCGCCGAGAGCTTCTGACACAGCCTCC 711
QY 3603 AGGGCTGTGGGAGCACTTGGGGCGTCAATGGAGCTTGGGCTACCCACTGCCCCAGC 3662
Db 712 AGGGCTGTGGGAGCACTTGGGGCGTCAATGGAGCTTGGGCTACCCACTGCCCCAGC 771
QY 3663 CGCTGCTGGGAGCTGAACCACTTGGACTTCTGGCTGCTGAAGAGCTGCAGACCTGGCTGCGGCCAAGG 3722
Db 772 CGCTGCTGGGAGCTGAACCACTTGGACTTCTGGCTGCTGAAGAGCTGCAGACCTGGCTGCGGCCAAGG 831
QY 3723 AGATGGAGCACTTCTGGCTGCTGAAGAGCTGCAGACCTGGCTGCGGCCAAGG 3782
Db 832 AGATGGAGCACTTCTGGCTGCTGAAGAGCTGCAGACCTGGCTGCGGCCAAGG 891
QY 3783 ACTTCAACCGCTCAAGAAAGATGAGAGCTCCAGAGCTGCAGTCAACCTGCACTGG 3842
Db 892 ACTTCAACCGCTCAAGAAAGATGAGAGCTCCAGAGCTGCAGTCAACCTGCACTGG 951
QY 3843 GGGCTCATGGCTTCTGCA 3859
Db 952 GGGCTCATGGCTTCTGCA 968

RESULT 11

US-09-864-761-23175/c
; Sequence 23175, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aemica-X-1
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203

; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 23175
; LENGTH: 495
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC005849.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 4.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.4
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4.2
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4.4
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4.5
; OTHER INFORMATION: SWISSPROT HIT: Q63086, EVALUE 8.00e-03
; OTHER INFORMATION: NT HIT: g111439486, EVALUE 0.00e+00
; OTHER INFORMATION: EST_HUMAN HIT: AI752561.1, EVALUE 0.00e+00
US-09-864-761-23175

Query Match 9.7%; Score 493.4; DB 9; Length 495;
Best Local Similarity 99.8%; Pred. No. 5.5e-134;
Matches 494; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3365 CTGAACCTACCTGGGCCCCCTTTCAACGAGCAGCAGCTTCAACCCCTCCCGCTGGGGCA 3424
DB 495 CTGAACCTACCTGGGCCCCCTTTCAACGAGCAGCAGCTTCAACCCCTCCCGCTGGGGCA 436
QY 3425 GAGACTCTGCGCAGGCGCCTGTGTGACTTGGAGGTGTGGAGGCTCAATGACAACTG 3484
DB 435 AAGACTCTGCGCAGGCGCCTGTGTGACTTGGAGGTGTGGAGGCTCAATGACAACTG 376
QY 3485 CGGCTGACCCAGAACTACGAGGCGCTACAGCCCTTCTGTGTACTTGGTGGCTCTCAAC 3544
DB 375 CGGCTGACCCAGAACTACGAGGCGCTACAGCCCTTCTGTGTACTTGGTGGCTCTCAAC 316
QY 3545 CGTCAGGCTGCCACTGCTGAGTGGCGCGCAGCTGCGCCCACTTCTGCAACGAGCTCCAG 3604
DB 315 CGTCAGGCTGCCACTGCTGAGTGGCGCGCAGCTGCGCCCACTTCTGCAACGAGCTCCAG 256
QY 3605 GCGCTCTGGGAGCTGCGGCGCTGCGGCGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGG 3664
DB 255 GCGCTCTGGGAGCTGCGGCGCTGCGGCGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGG 196
QY 3665 CTGCTCTGGGAGCTGAACCCCACTTGGACTCTGCGCCCTGCGCCCACTTCTGCAAG 3724
DB 195 CTGCTCTGGGAGCTGAACCCCACTTGGACTCTGCGCCCTGCGCCCACTTCTGCAAG 136
QY 3725 ATGGAGACTTCTGGCTGTCTGAAGGAGCTGCGAGCTGCGAGCTGCGGCTGCGGCTGCGG 3784
DB 135 ATGGAGACTTCTGGCTGTCTGAAGGAGCTGCGAGCTGCGAGCTGCGGCTGCGGCTGCGG 76
QY 3785 TTCAACCGGCTCAAGAGAGATGCGAGCTTCCAGCAGCTGCGAGCTGCGAGCTGCGAGCT 3844
DB 75 TTCAACCGGCTCAAGAGAGATGCGAGCTTCCAGCAGCTGCGAGCTGCGAGCTGCGAGCT 16
QY 3845 GCTCATGGCTTCTGA 3859
DB 15 GCTCATGGCTTCTGA 1

RESULT 12
US-10-296-115-607
; Sequence 607, Application US/10296115
; Publication No. US20040053248A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: No. US20040053248A1e1 Nucleic Acids and Polypeptides
; FILE REFERENCE: 784PCT
; CURRENT APPLICATION NUMBER: US/10/296,115
; CURRENT FILING DATE: 2002-11-18

; PRIOR APPLICATION NUMBER: US09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 1478
; SEQ ID NO 607
; LENGTH: 768
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-296-115-607
Query Match 9.7%; Score 492.4; DB 13; Length 768;
Best Local Similarity 99.8%; Pred. No. 1.4e-133;
Matches 493; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3363 AGCTGAACCTACCTGGGCCCCCTTTCAACGAGCAGCAGCTTCAACCCCTCCCGCTGGGG 3422
DB 275 ATCTGAACCTACCTGGGCCCCCTTTCAACGAGCAGCAGCTTCAACCCCTCCCGCTGGGG 334
QY 3423 CAGAGACTCTGCGCAGGCGCCTGTGTGACTTGGAGGTGTGGAGGCTCAATGACAAAC 3482
DB 335 CAGAGACTCTGCGCAGGCGCCTGTGTGACTTGGAGGTGTGGAGGCTCAATGACAAAC 394
QY 3483 TGGGCTGACCCAGAACTACGAGCCTACAGCCCTTCTGTGTACTTGGTGGCTTCA 3542
DB 395 TGGGCTGACCCAGAACTACGAGCCTACAGCCCTTCTGTGTACTTGGTGGCTTCA 454
QY 3543 ACCGTGAGGCTGCGCAGCTGCTGAGCTGCGCGCAGCCTTCTGTGCTGCTGCTGCTGCT 3602
DB 455 ACCGTGAGGCTGCGCAGCTGCTGAGCTGCGCGCAGCCTTCTGTGCTGCTGCTGCTGCT 514
QY 3603 AGGCGCTGCTGGGCGCAGCTTGGCGGCGTCTATGCGAGCTTGGGCTACCCACTGCGCCAGC 3662
DB 515 AGGCGCTGCTGGGCGCAGCTTGGCGGCGTCTATGCGAGCTTGGGCTACCCACTGCGCCAGC 574
QY 3663 CGCTGCGCTGGGACTGAACCCCACTTGGACTCTTGGGCTGCGCCAGCTGCTGCTGCTGCT 3722
DB 575 CGCTGCGCTGGGACTGAACCCCACTTGGACTCTTGGGCTGCGCCAGCTGCTGCTGCTGCT 634
QY 3723 AGATGAGCAGCTTCTGGCTGCTGAAAGAGCTGAGACCTTGGCTGCTGGCGCTGCGCCAGG 3782
DB 635 AGATGAGCAGCTTCTGGCTGCTGAAAGAGCTGAGACCTTGGCTGCTGGCGCTGCGCCAGG 694
QY 3783 ACTTCAACCGGCTCAGAGAGATGCGAGCTTCCAGCAGCTGCGAGCTGCGAGCTGCGAGCT 3842
DB 695 ACTTCAACCGGCTCAGAGAGATGCGAGCTTCCAGCAGCTGCGAGCTGCGAGCTGCGAGCT 754
QY 3843 GGGCTCATGGCTTC 3856
DB 755 GGGCTCATGGCTTC 768

RESULT 13
US-09-864-761-6462/c
; Sequence 6462, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aescima-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; CURRENT APPLICATION NUMBER: GB 24263.6

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; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 6462
; LENGTH: 492
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC005849.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 4.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.4
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4.2
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4.4
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4.5
; US-09-864-761-6462

Query Match
Best Local Similarity 9.7%; Score 492; DB 9; Length 492;
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3519 TTCTGTGTACTTGTGGTGGCTCAACCGTCAAGGCTGCGCTGAGTGGCGCGCAGCC 3578
Db 492 TTCTGTGTACTTGTGGTGGCTCAACCGTCAAGGCTGCGCTGAGTGGCGCGCAGCC 433
Qy 3579 TGGCCCACTTCTGACACAGCTCCAGGCTGCTGGGAGCATTGGGGGGTGTATGGAG 3638
Db 432 TGGCCCACTTCTGACACAGCTCCAGGCTGCTGGGAGCATTGGGGGGTGTATGGAG 373
Qy 3639 CTCTGGGCTACCCACTGCGCCAGCGCTGCTGGGAGCTGAACCCACTTGGACTCTTG3CC 3698
Db 372 CTCTGGGCTACCCACTGCGCCAGCGCTGCTGGGAGCTGAACCCACTTGGACTCTTG3CC 313
Qy 3699 CTGCCCCACAGTGACTTCTCCAGAAGATGGACGACTTCTGGCTGCTGAAGAGTGCAGA 3758
Db 312 CTGCCCCACAGTGACTTCTCCAGAAGATGGACGACTTCTGGCTGCTGAAGAGTGCAGA 253
Qy 3759 CTTGGCTGTGGCTCGGCCAGGACTTCAACCGCTCAAGAAGATGCAGCTCCAG 3818
Db 252 CTTGGCTGTGGCTCGGCCAGGACTTCAACCGCTCAAGAAGATGCAGCTCCAG 193
Qy 3819 CAGCTGCAGTCAACCTGCAGCTGGGGGCTCATGGCTTCTGACTTCTGACTTCTCTCTT 3878
Db 3878 CAGCTGCAGTCAACCTGCAGCTGGGGGCTCATGGCTTCTGACTTCTCTCTTCTCTCTT
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Qy 3939 TTGAGCCAGGAGACAGAGCTGTGAGCTCTTGCCCTTTCTTGAGCCGGCTGGGCGTGTG 3998
Db 72 TTGAGCCAGGAGACAGAGCTGTGAGCTCTTGCCCTTTCTTGAGCCGGCTGGGCGTGTG 13
Qy 3999 ATGCGATCAGCC 4010
Db 12 ATGCGATCAGCC 1

RESULT 14
US-09-867-701-4667
; Sequence 4667, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Agiate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4667
; LENGTH: 465
; TYPE: DNA
; ORGANISM: Homo sapien
; US-09-867-701-4667

Query Match
Best Local Similarity 8.6%; Score 437.2; DB 9; Length 465;
Matches 461; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

Qy 133 CAGGTTGAAACCCAAACTAGCCCTGCTCTTATATACATGACAGCAGCGCCCATCTGA 192
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Search completed: August 16, 2004, 10:40:07
Job time : 2944.55 secs

RESULT 15
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; Sequence 4, Application US/09931704
; Patent No. US20020041873A1
; GENERAL INFORMATION:
; APPLICANT: Senaldi, Giorgio
; TITLE OF INVENTION: Methods and Compositions for Treating IgE-Related Disease Using N
; TITLE OF INVENTION: Inhibitors
; FILE REFERENCE: A-695
; CURRENT APPLICATION NUMBER: US/09/931,704
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: US 60/226,436
; PRIOR FILING DATE: 2000-08-18
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 819
; TYPE: DNA
; ORGANISM: Murine
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (95)..(769)
; OTHER INFORMATION:
; NAME/KEY: mat_peptide
; LOCATION: (176)..()
; OTHER INFORMATION:
; NAME/KEY: mat_peptid
; LOCATION: (176)..(769)
; OTHER INFORMATION:
; NAME/KEY: sig_peptide
; LOCATION: (95)..(175)
; OTHER INFORMATION:
; US-09-931-704-4

Query Match		8.4%;	Score 429.6;	DB 9;	Length 819;
Best Local Similarity		90.4%;	Pred. No. 4.6e-115;		
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Db	576	CTTGCCAGGAGCTGAGCCAGCCTGGGCCCCCTGGCCCACTGAGTACTTCTCTCCAGA	635		
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Qy	3783	ACTTCAACCGGCTCAAGAAAGATGAGGCTCCAGAGCTGAGTCAACCTGACCTGG	3842		
Db	696	ACTTCAACCGGCTTAAGAAAGATGAGGCTCCAGAGCTTCAAGAGCTTCAAGTCACTGG	755		
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RESULT 2

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; Sequence 3, Application US/0898819
; Patent No. 6054294
; GENERAL INFORMATION:
; APPLICANT: CHANG, MING-SHI
; TITLE OF INVENTION: NEUTROTROPIC FACTOR NNT-1
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMGEN INC.
; STREET: ONE AMGEN CENTER DRIVE
; CITY: THOUSAND OAKS
; STATE: CA
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/988,819
; FILING DATE: 12-DEC-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/792,019
; FILING DATE: 03-FEB-1997
; ATTORNEY/AGENT INFORMATION:
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; NAME: COOK, ROBERT R.
; REGISTRATION NUMBER: 31,602
; REFERENCE/DOCKET NUMBER: A-442A
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5087 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 137..138
; OTHER INFORMATION: /product= "INTERVENING UNSEQUENCED
; OTHER INFORMATION: REGION OF >1KB"
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US-08-988-819-3
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Query Match 100.0%; Score 5087; DB 3; Length 5087;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5087; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACCTGGAGTGGGCTGCGGATGGGATTTAAAGCTTCGCGGAGCGCGGCTCGCC 60
Db 1 AACCTGGAGTGGGCTGCGGATGGGATTTAAAGCTTCGCGGAGCGCGGCTCGCC 60
QY 61 CTCCTCATCCGAGGCTCCGAGAGAGGAGCCGACCCCGGCGGCGGAGCGGCGGCA 120
Db 61 CTCCTCATCCGAGGCTCCGAGAGAGGAGCCGACCCCGGCGGCGGAGCGGCGGCA 120
QY 121 TGGACCTCCGAGGAGGTTGAAACCCAACTAGCCCTGCTCTTTCATAAATGACAAAGCAG 180
Db 121 TGGACCTCCGAGGAGGTTGAAACCCAACTAGCCCTGCTCTTTCATAAATGACAAAGCAG 180
QY 181 CGCCCCATCTGATACCTTAAACCGACCAAGTCACAGCCCTCAAACCTCAACCTTGCCTGCC 240
Db 181 CGCCCCATCTGATACCTTAAACCGACCAAGTCACAGCCCTCAAACCTCAACCTTGCCTGCC 240
QY 241 CAGACCTCACACATCTTGTGGACTCAAACTCAACCGGCTCAAACTCAACCTTGCCTGCC 300
Db 241 CAGACCTCACACATCTTGTGGACTCAAACTCAACCGGCTCAAACTCAACCTTGCCTGCC 300
QY 301 AGTCTAAACTAACTGAAACTTTTAAAGTAAACCCAGTCTTAAACCTTAAACCTAGCCCAAT 360
Db 301 AGTCTAAACTAACTGAAACTTTTAAAGTAAACCCAGTCTTAAACCTTAAACCTAGCCCAAT 360
QY 361 GCCAATTATATCTACCTAGCCAAACCCCTTAACCTTTCGCGAGTCCAAAGTGTCCACTG 420
Db 361 GCCAATTATATCTACCTAGCCAAACCCCTTAACCTTTCGCGAGTCCAAAGTGTCCACTG 420
QY 421 AATCCTCACCTTGGTCTCTCACTGAAATCCAGAAAGCATATTTCCCACTGCCACAT 480
Db 421 AATCCTCACCTTGGTCTCTCACTGAAATCCAGAAAGCATATTTCCCACTGCCACAT 480
QY 481 CCCTCTTTACAGCACCACCCCTGGCTCTGGACTCTGGTATCTCTGGTATCTCTGGTATCTCTGGT 540
Db 481 CCCTCTTTACAGCACCACCCCTGGCTCTGGACTCTGGTATCTCTGGTATCTCTGGTATCTCTGGT 540
QY 541 CTGCAGTGGCATCAGCCCAAGCCGACTCGTCAAAATGACCTCTCTCCCTTCTCTGTCTCC 600
Db 541 CTGCAGTGGCATCAGCCCAAGCCGACTCGTCAAAATGACCTCTCTCCCTTCTCTGTCTCC 600
QY 601 CCACCTTTCAGGCTGATGGAAGGCGCTCATTTGAAGTCCAACTTTTCCCACTAACACC 660
Db 601 CCACCTTTCAGGCTGATGGAAGGCGCTCATTTGAAGTCCAACTTTTCCCACTAACACC 660
QY 661 AAGAACGGGTGAGACCTCCACACTGCCACCGTTCCCTGAGAGTGAGCAGCTAAATCTCCTT 720
Db 661 AAGAACGGGTGAGACCTCCACACTGCCACCGTTCCCTGAGAGTGAGCAGCTAAATCTCCTT 720
QY 721 CAATCTAACCCCACTTACACTTTCCCACTCAGGAATCACTCTTAGAATATATACCCAAA 780
Db 721 CAATCTAACCCCACTTACACTTTCCCACTCAGGAATCACTCTTAGAATATATACCCAAA 780
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QY	1	AACCTCGAGTGGGCTGCGGATGGGATTATTAAGCTTCGCGGAGCCGCGCTCGCC	60
Db	1	AACCTCGAGTGGGCTGCGGATGGGATTATTAAGCTTCGCGGAGCCGCGCTCGCC	60
QY	61	CTCCCACTCCGCGAGGCTCCGGAGAGGAGCGCACCCGGCGGCGCCAGCCCCCA	120
Db	61	CTCCCACTCGGCGAGCTCCGGAGAGGAGCGCACCCGGCGGCGCCAGCCCCCA	120
QY	121	TGGACCTCGGAGAGGTTGAATAACCAACTAGCCCTGCTTTATATACATGACAAGCAG	180
Db	121	TGGACCTCCGAGCAGGTTGAATAACCAACTAGCCCTGCTTTCTATAACATGACAAGCAG	180
QY	181	CGGCCCCATCTGTATACCTAAACCGACCAAGTCAAGCCCTCCAACTCAACCTCTGCCTGCC	240
Db	181	CGGCCCCATCTGTATACCTAAACCGACCAAGTCAAGCCCTCCAACTCAACCTCTGCCTGCC	240
QY	241	CAGACCTCCACCATCCTGTGGAGTCAAACTCAACCGCACTAAATCAACCAATCCCA	300
Db	241	CAGACCTCACCATCCTGTGGAGTCAAACTCAACCGCACTAAATCAACCAATCCCA	300
QY	301	AGTCTAAACTAATCTGAAGCTTTTAAAGTAAACCCAGTCTTTAAACCTTAACCTAGCCCAAT	360
Db	301	AGTCTAAACTAATCTGAAGCTTTTAAAGTAAACCCAGTCTTTAAACCTTAACCTAGCCCAAT	360

Db 1441 CACAGGGACCCAGGGCCCTGGCCCTTCATCCAGAAACCTATGACCTCAACCGGTACTT 1500
QY 1501 GGAGCACCACCTCCGAGCTTGGCTGGGACCTATGTAGTATCCAGCGTAGGAATCTGGG 1560
Db 1501 GGAGCACCACCTCCGAGCTTGGCTGGGACCTATGTAGTATCCAGCGTAGGAATCTGGG 1560
QY 1561 AGTGGGAGGAGTGGAGGATGGGGAAGAAGTCTTAAACCGTGGAGGGTCTGGTAAA 1620
Db 1561 AGTGGGAGGAGTGGAGGATGGGGAAGAAGTCTTAAACCGTGGAGGGTCTGGTAAA 1620
QY 1621 TGATGGGGTGGAGAGGGGCTTTTGGCTCCCACTGCTCCCTGCTGCTGCTATCTCCTG 1680
Db 1621 TGATGGGGTGGAGAGGGGCTTTTGGCTCCCACTGCTCCCTGCTGCTGCTATCTCCTG 1680
QY 1681 CCTTCCCTCTTAGGTGGCCGCCCACTTCCCATCTCTGGCCCGCAGGACTAGGCATGTG 1740
Db 1681 CCTTCCCTCTTAGGTGGCCGCCCACTTCCCATCTCTGGCCCGCAGGACTAGGCATGTG 1740
QY 1741 GGCAGGCTCGACCCGCTTGGCCCATTTGCCCACTTGGCCCACTTGGCTGGCCCGCCGCC 1800
Db 1741 GGCAGGCTCGACCCGCTTGGCCCATTTGCCCACTTGGCCCACTTGGCTGGCCCGCCGCC 1800
QY 1801 TCCCTCTGGGGCGGGGAAGTCTCTCTGTTTACACCGTGTGTGTGTCTCTTGGCGG 1860
Db 1801 TCCCTCTGGGGCGGGGAAGTCTCTCTGTTTACACCGTGTGTGTGTCTCTTGGCGG 1860
QY 1861 GCGGGGTTGGGTGGGACAGAGGGGCCCACTCCCATCTGCTGCTTCCAGCTCGCCTC 1920
Db 1861 GCGGGGTTGGGTGGGACAGAGGGGCCCACTCCCATCTGCTGCTTCCAGCTCGCCTC 1920
QY 1921 TGCCCTCAGACCTGGGGCCCTGCTCTGTAACCCAGGGGCTTCCCTTCCGCTGCTCT 1980
Db 1921 TGCCCTCAGACCTGGGGCCCTGCTCTGTAACCCAGGGGCTTCCCTTCCGCTGCTCT 1980
QY 1981 CCATCTAGCTGGGCTCTAGGGGGTCTAGGGGGTCTAGGGGGTCTAGGGGGTCTAGGG 2040
Db 1981 CCATCTAGCTGGGCTCTAGGGGGTCTAGGGGGTCTAGGGGGTCTAGGGGGTCTAGGG 2040
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Db 2041 CAGTGTGGCAGGGGTTTAGGGTGTGGATGGAGTTATGCTGTAAAGATTTGGGGGTG 2100
QY 2101 TCAGAGGTTTCAGAGCCCAAGGACAGAGAGGAGGTTTGGAGGACCGAGGCACC 2160
Db 2101 TCAGAGGTTTCAGAGCCCAAGGACAGAGAGGAGGTTTGGAGGACCGAGGCACC 2160
QY 2161 ATGGGAAACCGGCCCTCTTCCCTGTTCTCTTCCACATCCAGACCTTACTCTGGAG 2220
Db 2161 ATGGGAAACCGGCCCTCTTCCCTGTTCTCTTCCACATCCAGACCTTACTCTGGAG 2220
QY 2221 CCAAGGAAAGAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2280
Db 2221 CCAAGGAAAGAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2280
QY 2281 AGGAAATTTAGTTGTCTGTGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2340
Db 2281 AGGAAATTTAGTTGTCTGTGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2340
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Db 2341 TCCAGGCTCTCCCTTGTCTTCCCTTGTCTTCCAGTTATACATCTCCCTCATCCCTT 2400
QY 2401 TCCCTGGGCGGACCGCTCCCGAGGTTGAAAGGGTCTGCGCTCTTCCCTATACC 2460
Db 2401 TCCCTGGGCGGACCGCTCCCGAGGTTGAAAGGGTCTGCGCTCTTCCCTATACC 2460
QY 2461 ATGTGTCTTCCATAGGCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2520
Db 2461 ATGTGTCTTCCATAGGCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2520
QY 2521 CTGCAACCTGCTCTATAGCTGAACCTTCTTCTGGAGTGTAGTGTAGTGTAGTGTAGTGT 2580

2521 CTGCAACCTGCTCTATAGCTGAACCTTCTTCTGGAGTGTAGTGTAGTGTAGTGTAGTGT 2580
2581 TCCCGAGCCCTCAGCTGTGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2640
2581 TCCCGAGCCCTCAGCTGTGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2640
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2701 CCTCTCTAGTTCGCAACCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2760
2701 CCTCTCTAGTTCGCAACCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2760
2761 GTGGTCTACACCTCTGCT 2820
2761 GTGGTCTACACCTCTGCT 2820
2821 TCTGGCTTCAGGGCCCGCAGCAATGGTGTCTCTCAAGGTGTGTGTGTGTGTGTGTGTGTGT 2880
2821 TCTGGCTTCAGGGCCCGCAGCAATGGTGTCTCTCAAGGTGTGTGTGTGTGTGTGTGTGTGT 2880
2881 CCGGACAGT 2940
2881 CCGGACAGT 2940
2941 CGGTGTGCTCTCTGCAACCT 3000
2941 CGGTGTGCTCTCTGCAACCT 3000
3001 CCTCTCAGCTCTCTCAGGCT 3060
3001 CCTCTCAGCTCTCTCAGGCT 3060
3061 CCAAGTGTTCGCAACCT 3120
3061 CCAAGTGTTCGCAACCT 3120
3121 CT 3180
3121 CT 3180
3181 ACCTGTGATCAAAATGATATCTTATTGGAATACTCAGGGAGGCTTGAACAAAGAGCC 3240
3181 ACCTGTGATCAAAATGATATCTTATTGGAATACTCAGGGAGGCTTGAACAAAGAGCC 3240
3241 TAGCATGGAGACAGGGCCAGTGTCTGAGGGACACAAAATAGAAAATTTTGGGAGGAGTA 3300
3241 TAGCATGGAGACAGGGCCAGTGTCTGAGGGACACAAAATAGAAAATTTTGGGAGGAGTA 3300
3301 TCTCTTGT 3360
3301 TCTCTTGT 3360
3361 ACAGTGAATCTACTGGGGCCCTTCAAGAGGCTTCAAGAGGCTTCAAGAGGCTTCAAGAGG 3420
3361 ACAGTGAATCTACTGGGGCCCTTCAAGAGGCTTCAAGAGGCTTCAAGAGGCTTCAAGAGG 3420
3421 GGCAGAGCTCTGCGGAGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3480
3421 GGCAGAGCTCTGCGGAGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3480
3481 ACTCGGCTGACCCAGAACTACAGGCTTACAGGCTTACAGGCTTACAGGCTTACAGGCTT 3540
3481 ACTCGGCTGACCCAGAACTACAGGCTTACAGGCTTACAGGCTTACAGGCTTACAGGCTT 3540
3541 CAAAGGCTGAGGCTGAGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3600
3541 CAAAGGCTGAGGCTGAGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3600
3601 CCAAGGCTGCTGTGGGAGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3660
3601 CCAAGGCTGCTGTGGGAGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3660

FEATURE:
 NAME/KEY: mat_peptide
 LOCATION: 127..720
 US-09-106-182-1

Query Match 28.8%; Score 1463.4; DB 3; Length 1710;
 Best Local Similarity 59.9%; Pred. No. 0;
 Matches 1464; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	3363	AGCTGAACCTACCTGGGCCCCCTTTCAACGAGCCAGACTTCAACCCCTCCCGCCCTGGGGG	3422
DB	227	ATCTGAACCTACCTGGGCCCCCTTTCAACGAGCCAGACTTCAACCCCTCCCGCCCTGGGG	286
QY	3423	CAGAGACTCTGCCCAGGGCCACTGTTGACTTGGAGGTGGGGAAGCCCTCAATGACAAC	3482
DB	287	CAGAGACTCTGCCCAGGGCCACTGTTGACTTGGAGGTGGGGAAGCCCTCAATGACAAC	346
QY	3483	TGCGGCTGACCCAGAACTAGAGGCTTACAGCCACTTCTGTGTTACTTGGCTGGCTCA	3542
DB	347	TGCGGCTGACCCAGAACTAGAGGCTTACAGCCACTTCTGTGTTACTTGGCTGGCTCA	406
QY	3543	ACCGTCAAGCTGCACTGTGAGCTGCGCGGAGCGCTGCGCCACTTGTGACACGCTCC	3602
DB	407	ACCGTCAAGCTGCACTGTGAGCTGCGCGGAGCGCTGCGCCACTTGTGACACGCTCC	466
QY	3603	AGGGCTGCTGGGAGCACTTGGGGGCTCATGGCAGCTCTGGGCTACCCACTGCCCCCAGC	3662
DB	467	AGGGCTGCTGGGAGCACTTGGGGGCTCATGGCAGCTCTGGGCTACCCACTGCCCCCAGC	526
QY	3663	CGCTGCTGGGAGTGAACCACTTGGACTCTTGGCCCTGCCACAGTGAATCTCTCCAGA	3722
DB	527	CGCTGCTGGGAGTGAACCACTTGGACTCTTGGCCCTGCCACAGTGAATCTCTCCAGA	586
QY	3723	AGATGACAGACTCTGGCTGTGAAGAGCTGAGACCTGTGCTGGCTGGGCTGGGCTGGG	3782
DB	587	AGATGACAGACTCTGGCTGTGAAGAGCTGAGACCTGTGCTGGCTGGGCTGGGCTGGG	646
QY	3783	ACTTCAACCGGCTCAAGAGAGAGTCAAGCTCCAGCAGCTGAGTCAACCTGCACTGG	3842
DB	647	ACTTCAACCGGCTCAAGAGAGAGTCAAGCTCCAGCAGCTGAGTCAACCTGCACTGG	706
QY	3843	GGGCTCATGGCTTCTGACTTCTGACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	3902
DB	707	GGGCTCATGGCTTCTGACTTCTGACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	766
QY	3903	CACCTTTGAGAGCCAGCCCTGATCCCAACACCTGTTGAGCCAGGAGACAGAAAGCTGT	3962
DB	767	CACCTTTGAGAGCCAGCCCTGATCCCAACACCTGTTGAGCCAGGAGACAGAAAGCTGT	826
QY	3963	AGCCTTGCGCCCTTCTCTGAGCGGCTGGGCTGTGATCGATCGACCTGCTCTCTCC	4022
DB	827	AGCCTTGCGCCCTTCTCTGAGCGGCTGGGCTGTGATCGATCGACCTGCTCTCTCC	886
QY	4023	CACCTCCCAAGGCTACCGAGCTGGGAGGAGTACAGTAGGCGCTGCTCTCTCTCT	4082
DB	887	CACCTCCCAAGGCTACCGAGCTGGGAGGAGTACAGTAGGCGCTGCTCTCTCTCT	946
QY	4083	TCTACAGGAAGTCACTGCTCGAGGAGTGTGAAGTGGTTTCAGGTGGTGAGAGGGCTCA	4142
DB	947	TCTACAGGAAGTCACTGCTCGAGGAGTGTGAAGTGGTTTCAGGTGGTGAGAGGGCTCA	1006
QY	4143	TGGCTCTGCT	4202
DB	1007	TGGCTCTGCT	1066
QY	4203	TCTGAGGGGAGGGGTTGAGGGGCCCCACACACATGCTTCTTGGGCTGAAGCCCTTT	4262
DB	1067	TCTGAGGGGAGGGGTTGAGGGGCCCCACACACATGCTTCTTGGGCTGAAGCCCTTT	1126
QY	4263	GGCTGCCCCACTCTCTCTGAGTGGGTGTGCTCCCTTATCCCAATCACTATACATC	4322
DB	1127	GGCTGCCCCACTCTCTCTGAGTGGGTGTGCTCCCTTATCCCAATCACTATACATC	1186

QY	4323	CAATTAGGAAACAAACATGGTGGCAATTTCTACACAAAAGAGATGAGATTACAGTGA	4382
DB	1187	CAATTAGGAAACAAACATGGTGGCAATTTCTACACAAAAGAGATGAGATTACAGTGA	1246
QY	4383	GGGTTGGGCTCTGCTATTGGAGGTGCCCTATAAAACCAAGAGAGAAATATCTGAAAGCACAG	4442
DB	1247	GGGTTGGGCTCTGCTATTGGAGGTGCCCTATAAAACCAAGAGAGAAATATCTGAAAGCACAG	1306
QY	4443	GGGAGGGAAGACCCAGACCCAGAGAGTCTCCAAAGCAAGAGTGGCAAAACAAAC	4502
DB	1307	GGGAGGGAAGACCCAGACCCAGAGAGTCTCCAAAGCAAGAGTGGCAAAACAAAC	1366
QY	4503	CCGAGCTGAGCATCAGGACCTTGCCTGGAATTCCTTCCAGTATTACGGTGCCTCTTCTC	4562
DB	1367	CCGAGCTGAGCATCAGGACCTTGCCTGGAATTCCTTCCAGTATTACGGTGCCTCTTCTC	1426
QY	4563	TGCCCCCTTTCCAGGATATCTGTGGTTGCCAGGTGGGAGGGCAACCATAGCCACAC	4622
DB	1427	TGCCCCCTTTCCAGGATATCTGTGGTTGCCAGGTGGGAGGGCAACCATAGCCACAC	1486
QY	4623	CACAGGATTTCTTGAAGTTTACAATGCAGTAGCATTTTGGGGTGGAGTGGCAGCTCC	4682
DB	1487	CACAGGATTTCTTGAAGTTTACAATGCAGTAGCATTTTGGGGTGGAGTGGCAGCTCC	1546
QY	4683	CCAAGGCCCTGCCCCCCCCCAGCCCAACCCACCTCATGACTCTAAGTGTGTGTATTATTT	4742
DB	1547	CCAAGGCCCTGCCCCCCCCCAGCCCAACCCACCTCATGACTCTAAGTGTGTGTATTATTT	1606
QY	4743	ATTATTGGAGATGTTATTATTATAGATATATTATTCAGAAATTTCTATTCTTCTTATT	4802
DB	1607	ATTATTGGAGATGTTATTATTATAGATATATTATTCAGAAATTTCTATTCTTCTTATT	1666
QY	4803	AACAAATAAAATGCTTGCCCCAGAA	4827
DB	1667	AACAAATAAAATGCTTGCCCCAGAA	1691

RESULT 5
 US-08-792-019B-1
 ; Sequence 1, Application US/08792019B
 ; Patent No. 5741772
 ; GENERAL INFORMATION:
 ; APPLICANT: CHANG, MING-SHI
 ; TITLE OF INVENTION: THE NEUROTROPHIC FACTOR NNT-1
 ; NUMBER OF SEQUENCES: 16
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: AMGEN INC.
 ; STREET: 1840 DEHAVILLAND DRIVE
 ; CITY: THOUSAND OAKS
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 91320
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/792,019B
 ; FILING DATE: 03-FEB-1997
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: COOK, ROBERT R.
 ; REGISTRATION NUMBER: 31,602
 ; REFERENCE/DOCKET NUMBER: A-442
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 797 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; FEATURE: